

## Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model  
Run on: September 30, 2005, 10:05:32 ; Search time 86 Seconds  
(without alignments)  
1244.472 Million cell updates/sec

Title: US-09-980-758A-8  
Perfect score: 1045  
Sequence: 1 PRDLPNPREKMKSEKREL.....NFDIVNDEPLEGRYKWDRLX 209

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_03:\*  
1: uniprot\_prot:\*  
2: uniprot\_trebl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query %	Match	Length	ID	Description
1	969	92.7	196	2	Q9LJL5	Q9LJL5 arabidopsis
2	347.5	33.3	195	2	Q94CL9	Q94CL9 arabidopsis
3	346.5	33.2	195	2	Q9FX90	Q9FX90 arabidopsis
4	285	27.3	60	2	Q8W2K3	Q8W2K3 arabidopsis
5	187	17.9	192	2	Q9FS28	Q9FS28 pisum sativ
6	179	17.1	166	2	Q6T2Z0	Q6T2Z0 glycine max
7	179	17.1	207	2	Q8GUA2	Q8GUA2 nicotiana t
8	177	16.9	209	2	Q9SCR2	Q9SCR2 arabidopsis
9	176.5	16.9	191	2	O04154	O04154 arabidopsis
10	175.5	16.8	191	2	O82809	O82809 arabidopsis
11	175.5	16.8	191	2	O8LXD1	O8LXD1 arabidopsis
12	172	16.5	286	2	Q94CM0	Q94CM0 arabidopsis
13	169	16.2	205	2	Q6T2Z3	Q6T2Z3 glycine max
14	168.5	16.1	196	2	O48597	O48597 chenopodium
15	167	16.0	286	2	Q8GJY3	Q8GJY3 arabidopsis
16	164.5	15.7	185	2	Q8GT28	Q8GT28 lycopersico
17	162.5	15.6	289	2	O48846	O48846 arabidopsis
18	161.5	15.4	198	2	Q6T2Z2	Q6T2Z2 glycine max
19	156.5	15.0	500	1	GAR2_SCHPO	P41891 schizosacch
20	153.5	14.7	180	2	Q6T2Z1	Q6T2Z1 glycine max
21	153	14.6	262	2	Q6Z6G5	Q6Z6G5 oryza sativ
22	152	14.5	222	2	Q9FKB5	Q9FKB5 arabidopsis
23	145.5	13.9	210	2	Q8GT29	Q8GT29 lycopersico
24	144	13.8	242	2	Q7XDH8	Q7XDH8 oryza sativ
25	144	13.8	242	2	Q9FW65	Q9FW65 oryza sativ
26	143.5	13.7	396	2	Q754G3	Q754G3 ashbya goss
27	138.5	13.3	406	1	SR40_YEAST	P32583 saccharomyc
28	132.5	12.7	414	1	NSR1_YEAST	P27476 saccharomyc
29	132.5	12.7	451	2	Q9P785	Q9P785 schizosacch
30	132.5	12.7	2271	2	Q99QY4	Q99QY4 staphylococ
31	132.5	12.7	2271	2	Q7A362	Q7A362 staphylococ

32	131.5	12.6	1241	2	Q75JC0	Q75JC0 dictyosteli
33	131	12.5	412	2	Q6MF11	Q6MF11 neurospora
34	131	12.5	471	2	Q7RZG9	Q7RZG9 neurospora
35	130.5	12.5	371	2	Q6FTH7	Q6FTH7 candida gla
36	129.5	12.4	163	2	Q93V92	Q93V92 nicotiana t
37	128	12.2	156	2	Q93VF6	Q93VF6 nicotiana s
38	128	12.2	189	2	Q91RY0	Q91RY0 arabidopsis
39	128	12.2	600	2	Q90237	Q90237 anolis pulc
40	128	12.2	680	2	Q92033	Q92033 anolis pulc
41	127.5	12.2	455	2	Q86A18	Q86A18 dictyosteli
42	127	12.2	1444	2	Q9VTN2	Q9VTN2 drosophila
43	127	12.2	1514	2	Q8SY55	Q8SY55 drosophila
44	126.5	12.1	2275	2	O8NUJ3	O8NUJ3 staphylococ
45	126.5	12.1	2275	2	Q6G620	Q6G620 staphylococ

## ALIGNMENTS

### RESULT 1

Q9LJL5 PRELIMINARY; PRT; 196 AA.  
AC Q9LJL5  
DT 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)  
DE Gb|AAC23758.1 (Cyclin-dependent kinase inhibitor 6).  
GN Name=ACK1; Synonyms=krp6;  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC euroside II; Brassicales; Brassicaceae; Arabidopsi.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20363099; PubMed=10907853;  
RA Nakamura Y.;  
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.  
RT Sequence features of the regions of 4,251,695 bp covered by ninety Pl,  
RT TAC and BAC clones."  
RL DNA Res. 7:217-221(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;  
RN [3]  
RP Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Park S.C., Cho J.W.;  
RN [5]  
RP Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A.  
RA de Veylder L., Beeckman T., Beemster G.T.S., Krols L., Terras F.,  
RN [7]  
RP Landrieu I., Van Der Schueren E., Maes S., Naudts M., Inze D.;  
RT "Functional analysis of Cyclin-dependent kinase inhibitors of  
RT Arabidopsis."  
RL Plant Cell 13:1653-1668(2001).  
DR EMBL; AF000419; BAB02955.1; -;  
DR EMBL; AF106705; AAF77612.2; -;  
DR EMBL; AJ301557; CAC41620.1; -;  
DR GO; GO:0005634; Cinnuleus; IEA.  
DR GO; GO:0004861; F.cyclin-dependent protein kinase inhibitor a. . . ; IEA.  
DR GO; GO:0016301; F.kinase activity; IEA.  
DR GO; GO:0007050; P:cell cycle arrest; IEA.  
DR InterPro; IPR003175; CDI.  
DR Pfam; PF02334; CDI; 1.  
KW Cyclin; Kinase.  
SQ SEQUENCE 196 AA; 21454 MW; ACS43304CE5B92C4 CRC64;

Query Match 92.7%; Score 969; DB 2; Length 196;  
Best Local Similarity 99.5%; Pred. No. 1.4e-54;  
Matches 195; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 13 MSERKRELAEEASSTSFSPKTKTKLNDSSDPDSDHVDVIFAVSSSSVASSAALASDRCS 72
Db 1 MSERKRELAEEASSTSFSPKTKTKLNDSSDPDSDHVDVIFAVSSSSVASSAALASDRCS 60
QY 73 VTIGGEESDQSSISSGCGTSSKEIAKNSSFGVDLEDHQIETETETSTFTTSNFRKET 132
Db 61 VTIGGEESDQSSISSGCGTSSKEIAKNSSFGVDLEDHQIETETETSTFTTSNFRKET 120
QY 133 SPVSEGLGTTTTEMESSSATKRGKQGVKRTPTAAEIEDLFSESPDDKKQFIEKYNFD 192
Db 121 SPVSEGLGTTTTEMESSSATKRGKQGVKRTPTAAEIEDLFSESPDDKKQFIEKYNFD 180
QY 193 INVDEPLEGRYKWDRL 208
Db 181 INVDEPLEGRYKWDRL 196
RESULT 2
ID Q94CL9 PRELIMINARY; PRT; 195 AA.
AC Q94CL9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cyclin-dependent kinase inhibitor 7.
GN Name=kfp7;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21342510; PubMed=11449057;
RA de Veylder L., Beeckman T., Bemster G.T.S., Krols L., Terras F.,
RA Landrieu I., Van der Schueren E., Maes S., Naudts M., Inze D.;
RT "Functional analysis of Cyclin-dependent kinase inhibitors of
RT Arabidopsis.";
RL Plant Cell 13:1653-1668(2001).
DR EMBL; AJ301558; CAC41621.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. . .; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0007050; P:cell cycle arrest; IEA.
DR InterPro; IPR003175; CDI.
DR Pfam; PF02234; CDI; 1.
KW Cyclin; Kinase.
SQ SEQUENCE 195 AA; 2208 MW; 60B81B47B752F6DF CRC64;
Query Match 33.3%; Score 347.5; DB 2; Length 195;
Best Local Similarity 45.4%; Pred. No. 8e-15;
Matches 93; Conservative 28; Mismatches 57; Indels 27; Gaps 10;
QY 13 MSERKRELAEEASSTSFSPKTKTKLNDSSD--SSPDSDHVDVIFAVSSSSVASSAALASDE 70
Db 1 MSETKPKRDSYEG--SNIKMRLLDDDDVLVRPTR-----TLSSSSSSSLAYSVD 51
QY 71 ---CSVTIGGEESD-QSSISSGCGTSSKEIAKNSSFGVDLEDHQIETETSTFTTS 126
Db 52 GGFCVALSEEDDHLSSISGCGSSSETNEIATLPF--SDLEAHEI-SETEISTLLTN 108
QY 127 NFRKETSVPSEGLGET-----TTMESSSATKRGKQGVKRTPTAAEIEDLFSESPDD 180
Db 109 NFRKQGISSENGLGTAEMDSATTEMRDQRKTEKKK-MEKSPTQAEILDFFSAAERYE- 166
QY 181 KKKQFIEKYNFIDVNDPLEGRYK 205
Db 167 -QKRFTKYNIDVNDTPLEGRYQW 190
RESULT 3
Q9FX90
ID Q9FX90 PRELIMINARY; PRT; 195 AA.
AC Q9FX90;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE F14J22.14 protein.
GN Name=F14J22.14;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21342510; PubMed=11449057;
RA de Veylder L., Beeckman T., Bemster G.T.S., Krols L., Terras F.,
RA Landrieu I., Van der Schueren E., Maes S., Naudts M., Inze D.;
RT "Functional analysis of Cyclin-dependent kinase inhibitors of
RT Arabidopsis.";
RL Plant Cell 13:1653-1668(2001).
DR EMBL; AJ301558; CAC41621.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. . .; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0007050; P:cell cycle arrest; IEA.
DR InterPro; IPR003175; CDI.
DR Pfam; PF02234; CDI; 1.
KW Cyclin; Kinase.
SQ SEQUENCE 195 AA; 2208 MW; 60B81B47B752F6DF CRC64;
Query Match 33.3%; Score 347.5; DB 2; Length 195;
Best Local Similarity 45.4%; Pred. No. 8e-15;
Matches 93; Conservative 28; Mismatches 57; Indels 27; Gaps 10;
QY 13 MSERKRELAEEASSTSFSPKTKTKLNDSSD--SSPDSDHVDVIFAVSSSSVASSAALASDE 70
Db 1 MSETKPKRDSYEG--SNIKMRLLDDDDVLVRPTR-----TLSSSSSSSLAYSVD 51
QY 71 ---CSVTIGGEESD-QSSISSGCGTSSKEIAKNSSFGVDLEDHQIETETSTFTTS 126
Db 52 GGFCVALSEEDDHLSSISGCGSSSETNEIATLPF--SDLEAHEI-SETEISTLLTN 108
QY 127 NFRKETSVPSEGLGET-----TTMESSSATKRGKQGVKRTPTAAEIEDLFSESPDD 180
Db 109 NFRKQGISSENGLGTAEMDSATTEMRDQRKTEKKK-MEKSPTQAEILDFFSAAERYE- 166
QY 181 KKKQFIEKYNFIDVNDPLEGRYK 205
Db 167 -QKRFTKYNIDVNDTPLEGRYQW 190
RESULT 4
Q9W2K3
ID Q9W2K3 PRELIMINARY; PRT; 60 AA.
AC Q9W2K3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cyclin-dependent kinase inhibitor p22ack1 (Fragment).
GN Name=ACK1;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21342510; PubMed=11449057;
RA de Veylder L., Beeckman T., Bemster G.T.S., Krols L., Terras F.,
RA Landrieu I., Van der Schueren E., Maes S., Naudts M., Inze D.;
RT "Functional analysis of Cyclin-dependent kinase inhibitors of
RT Arabidopsis.";
RL Plant Cell 13:1653-1668(2001).
DR EMBL; AJ301558; CAC41621.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. . .; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0007050; P:cell cycle arrest; IEA.
DR InterPro; IPR003175; CDI.
DR Pfam; PF02234; CDI; 1.
KW Cyclin; Kinase.
SQ SEQUENCE 60 AA; 6268 MW; D0DE7D7DBD0472A1 CRC64;

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AC Q9FX90;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE F14J22.14 protein.
GN Name=F14J22.14;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21342510; PubMed=11449057;
RA de Veylder L., Beeckman T., Bemster G.T.S., Krols L., Terras F.,
RA Landrieu I., Van der Schueren E., Maes S., Naudts M., Inze D.;
RT "Functional analysis of Cyclin-dependent kinase inhibitors of
RT Arabidopsis.";
RL Plant Cell 13:1653-1668(2001).
DR EMBL; AJ301558; CAC41621.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. . .; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0007050; P:cell cycle arrest; IEA.
DR InterPro; IPR003175; CDI.
DR Pfam; PF02234; CDI; 1.
SQ SEQUENCE 195 AA; 21965 MW; 6A7E0867B752E5FF CRC64;
Query Match 33.2%; Score 346.5; DB 2; Length 195;
Best Local Similarity 45.4%; Pred. No. 9.2e-15;
Matches 93; Conservative 27; Mismatches 58; Indels 27; Gaps 10;
QY 13 MSERKRELAEEASSTSFSPKTKTKLNDSSD--SSPDSDHVDVIFAVSSSSVASSAALASDE 70
Db 1 MSETKPKRDSYEG--SNIKMRLLDDDDVLVRPTR-----TLSSSSSSSLAYSVD 51
QY 71 ---CSVTIGGEESD-QSSISSGCGTSSKEIAKNSSFGVDLEDHQIETETSTFTTS 126
Db 52 GGFCVALSEEDDHLSSISGCGSSSETNEIATLPF--SDLEAHEI-SETEISTLLTN 108
QY 127 NFRKETSVPSEGLGET-----TTMESSSATKRGKQGVKRTPTAAEIEDLFSESPDD 180
Db 109 NFRKQGISSENGLGTAEMDSATTEMRDQRKTEKKK-MEKSPTQAEILDFFSAAERYE- 166
QY 181 KKKQFIEKYNFIDVNDPLEGRYK 205
Db 167 -QKRFTKYNIDVNDTPLEGRYQW 190
RESULT 4
Q9W2K3
ID Q9W2K3 PRELIMINARY; PRT; 60 AA.
AC Q9W2K3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cyclin-dependent kinase inhibitor p22ack1 (Fragment).
GN Name=ACK1;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21342510; PubMed=11449057;
RA de Veylder L., Beeckman T., Bemster G.T.S., Krols L., Terras F.,
RA Landrieu I., Van der Schueren E., Maes S., Naudts M., Inze D.;
RT "Functional analysis of Cyclin-dependent kinase inhibitors of
RT Arabidopsis.";
RL Plant Cell 13:1653-1668(2001).
DR EMBL; AJ301558; CAC41621.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. . .; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0007050; P:cell cycle arrest; IEA.
DR InterPro; IPR003175; CDI.
DR Pfam; PF02234; CDI; 1.
KW Cyclin; Kinase.
SQ SEQUENCE 60 AA; 6268 MW; D0DE7D7DBD0472A1 CRC64;

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Query Match 27.3%; Score 285; DB 2; Length 60;  
Best Local Similarity 100.0%; Pred. No. 1.9e-11;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 MSERKRELAEEASTSFSPKTKTKLNDSSDSSPDSDHVDIVFAVSSSSVASSAALASDECS 72  
DB 1 MSERKRELAEEASTSFSPKTKTKLNDSSDSSPDSDHVDIVFAVSSSSVASSAALASDECS 60

RESULT 5  
QFS28 ID QFS28 PRELIMINARY; PRT; 192 AA.  
AC QFS28;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Cyclin dependent kinase inhibitor.  
GN Name=Cki;  
OS Pisum sativum (Garden pea).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.  
OX NCBI\_TaxID=3888;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Axillary bud;  
RA Shimizu-Sato S., Mori H.;  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
RE EMBL; AB029483; BAB20860.1; -;  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. . .; IEA.  
DR GO; GO:0016301; P:kinase activity; IEA.  
DR GO; GO:0007050; P:cell cycle arrest; IEA.  
DR InterPro; IPR003175; CDI.  
DR Pfam; PF02234; CDI; 1.  
KW Cyclin; Kinase.  
SQ SEQUENCE 192 AA; 21921 MW; E76D734000885EB2 CRC64;

Query Match 17.9%; Score 187; DB 2; Length 192;  
Best Local Similarity 30.7%; Pred. No. 0.00014;  
Matches 59; Conservative 30; Mismatches 83; Indels 20; Gaps 6;

QY 20 LAEEASTSFSPKTKTKLNDSSDSSPDSDHVDIVFAVSSSSVAS--SAALASDCSVTIGG 77  
DB 16 LAEEASTSFSPKTKTKLNDSSDSSPDSDHVDIVFAVSSSSVAS--SAALASDCSVTIGG 67

QY 78 EESDQSSISSGCGTSESKEIAKNSGSGVGLDHDQIETETSTFTTSNFRKETSQVSE 137  
DB 68 EEPFASCCSNGSVELDEERIK-----SLDLEVASAQGTSTCNCDDEEREMRSSE 121

QY 138 GLGETTEMESSEATKRKQ-PGVRKTPATAAEIEDLFSELESPPDDKKQKQFIEKYNFDIVND 196  
DB 122 FRG-NGSHELESMTNSRRPISPPKTPTEYLESEFFAAAEK--DIQKKFQEKYNYDILKD 178

QY 197 EPLEGYKNDRL 208  
DB 179 VPLEGYEWVOL 190

RESULT 6  
Q6T220 ID Q6T220 PRELIMINARY; PRT; 166 AA.  
AC Q6T220;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Cyclin-dependent kinase inhibitor 2;2 (Fragment).  
OS Glycine max (Soybean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
OX NCBI\_TaxID=3847;  
RN [1]

RP SEQUENCE FROM N.A.  
RA Li S., Reverdatto S., Nielsen N.C.;  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
RE EMBL; AY439104; AAS13377.1; -;  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. . .; IEA.  
DR GO; GO:0016301; P:kinase activity; IEA.  
DR GO; GO:0007050; P:cell cycle arrest; IEA.  
DR InterPro; IPR003175; CDI.  
DR Pfam; PF02234; CDI; 1.  
KW Cyclin; Kinase.  
SQ SEQUENCE 166 AA; 18850 MW; 40FB19CF72A8A640 CRC64;

Query Match 17.1%; Score 179; DB 2; Length 166;  
Best Local Similarity 34.9%; Pred. No. 0.00039;  
Matches 60; Conservative 28; Mismatches 58; Indels 26; Gaps 10;

QY 40 SPDSSPDSDHVDIVFAVSSSSVASSAALASDECSVTIGGESDSSISGCGTSESKEIA 99  
DB 18 ASASSPRKRKISFVQKSLSNATSP--TTEE---RISG-ESPASCCSNGSFDNENR-II 70

QY 100 KNSSESFGVDLEDHQIETET-ETSTFTTSNFRKETSQVSEGLGETTEMESSE--ATKRKQ 156  
DB 71 KSSD---LEVESAQVETWTCNCGEQQQKIRREMS-----LTREVDSTEEHITKTS 119

QY 157 PGVRKTPATAAEIEDLFSELESPPDDKKQKQFIEKYNFDIVNDEPLEGKYKNDRL 208  
DB 120 ---RCVPTSELEDFFAAAEK--DIQKRTDKYNYDFVKDMPLEGYEWVOL 166

RESULT 7  
Q8GUA2 ID Q8GUA2 PRELIMINARY; PRT; 207 AA.  
AC Q8GUA2;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Cyclin-dependent kinase inhibitor.  
GN Name=Kis2;  
OS Nicotiana tabacum (Common tobacco).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC Lamiales; Solanales; Solanaceae; Nicotiana.  
OX NCBI\_TaxID=4097;  
RN [1]

RP SEQUENCE FROM N.A.  
RA Jasinski S., Saraiva Leite C., Domenichini S., Stevens R., Raynaud C.,  
RA Peremes C., Bergounioux C., Glab N.;  
RT "Ntkis2, a novel tobacco cyclin-dependent kinase inhibitor  
RT differentially expressed during the cell cycle and plant  
RT development.";  
RL Plant Physiol. Biochem. 41:667-676(2003).  
DR EMBL; AJ517189; CAD56868.1; -;  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. . .; IEA.  
DR GO; GO:0016301; P:kinase activity; IEA.  
DR GO; GO:0007050; P:cell cycle arrest; IEA.  
DR InterPro; IPR003175; CDI.  
DR Pfam; PF02234; CDI; 1.  
KW Cyclin; Kinase.  
SQ SEQUENCE 207 AA; 23278 MW; F5AE70AD2261BC2D CRC64;

Query Match 17.1%; Score 179; DB 2; Length 207;  
Best Local Similarity 28.6%; Pred. No. 0.00051;  
Matches 58; Conservative 30; Mismatches 81; Indels 34; Gaps 8;

QY 11 KXMSERKRELAEEASTSFSPKTKTKLNDSS--DSSPD-----SHDVIVFAVSSSSVASSA 64  
DB 28 KMTASAEREVLVADHA-----KKRKCQDGLMLPTVACVRSHSDILVAQESLVTPTS 82

QY 65 ALASDECSVTIGGESDSSISGCGTSESKEIAKNSGSGVGLDHDQIETETSTFTFI 124

DR	GO; GO:0007050; P:cell cycle arrest; IEA.	
DR	InterPro; IPR0031175; CDI.	
DR	Pfam; PF02234; CDI; 1.	
KW	Hypothetical protein.	
SQ	SEQUENCE 209 AA; 24036 MW; OE5EEFE9ED256B53 CRC64;	
Query Match 16.9%; Score 177; DB 2; Length 209;		
Best Local Similarity 30.7%; Pred. No. 0.0007;		
Matches 65; Conservative 44; Mismatches 73; Indels 30; Gaps 13;		
QY	16 RKRELAEEASSTFSFLKTKTKLNDSSDSPDGHVIVFAVSSSS---VASSAALASDEC 71	
DB	7 RERDVVEENGVTI-ITVRRKKEEVD-IVESRIILLSPCVQATNRGIVARNAGASETS 64	
QY	72 SVTIGGEES-----DQSSISSGCGFTSGSKEIAKNSSSGFVLDHQ-IETETET 120	
DB	65 VVIVRRDSPVPEEQCEEEDSSVSC-CSTSEK--SKRRIEF-VDLSEENGGDRETET 120	
QY	121 STFITSNFRKETSFVSEGLGETTETEMESSATKRGKQGVKTKPTAAEIEDLFSLESPDD 180	
DB	121 S-WIYDDLAK--SEESMNDSSSAVEDVESRRRLKSLHETVKEALEEDFFQVAEK--D 175	
QY	181 KKKQFTE--KYNFDIVNDEPL-EGRYKWDRL 208	
DB	176 LRNKLLLECKMKYNDFEKFDEPLGGRYEWVKL 207	
RESULT 9		
O04154	PRELIMINARY; PRT; 191 AA.	
ID	O04154	
AC	O04154;	
DT	01-JUL-1997 (TReMBLrel. 04, Created)	
DT	01-JUL-1997 (TReMBLrel. 04, Last sequence update)	
DT	01-JUN-2003 (TReMBLrel. 24, Last annotation update)	
DE	Cyclin-dependent kinase inhibitor protein.	
OS	Name-ICK1;	
OS	Arabidopsis thaliana (Mouse-ear cress).	
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;	
OC	eurosid II; Brassicales; Brassicaceae; Arabidopses.	
OX	NCBI_TaxID=3702;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=Columbia;	
RC	MEDLINE=97242401; PubMed=9087400;	
RA	Wang H., Fowke L.C., Crosby W.L.;	
RT	"A plant cyclin-dependent kinase inhibitor gene.";	
RL	Nature 386:451-452(1997).	
RL	EMBL; U94772; AAC49698.1; -.	
DR	GO; GO:0005634; C:nucleus; IEA.	
DR	GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. . ; IEA.	
DR	GO; GO:0016301; F:kinase activity; IEA.	
DR	GO; GO:0007050; P:cell cycle arrest; IEA.	
DR	InterPro; IPR0031175; CDI.	
DR	Pfam; PF02234; CDI; 1.	
KW	Cyclin; Kinase.	
SQ	SEQUENCE 191 AA; 22239 MW; 0432BD4F626C07B5 CRC64;	
Query Match 16.9%; Score 176.5; DB 2; Length 191;		
Best Local Similarity 26.7%; Pred. No. 0.00067;		
Matches 59; Conservative 34; Mismatches 63; Indels 65; Gaps 9;		
QY	16 RKRELAEEASSTFSFLKTKTKLNDSSDSPDGHVIVFAVSSSSVASSAALASDECSTVI 75	
DB	7 KAGIVEAGVSSITMQLRSR-----IVYRSEKS-----SSVSV 41	
QY	76 GGEEDQSSISSGCGFTSGSKEIAKNSSSGFVLDHQIETETSTF-----ITSNF 128	
DB	42 VGD-----NGVSSC--SGSNEYKKEL---IHLEEDKGDGTSTYRRGTRKKLCENL 91	
QY	129 RKE-----TSPVSEGL-----GETTEMSSATKRGKQGVKTKPTAAE 167	
DB	92 REEKEELKSMENYSSEFSAVKESLDCCSGRKTMEETVTAPEEESKAKLMTMPTESE 151	



de Veylder L., Beekman T., Beemster G.T.S., Krols L., Terras F., Landrieu I., Van Der Schueren E., Maes S., Naudts M., Inze D.; "Functional analysis of Cyclin-dependent kinase inhibitors of Arabidopsis"; Plant Cell 13:1653-1668 (2001).  
EMBL; AJ301555; CAC41618.1; -.  
GO: GO:0005634; C:nucleus; IEA.  
GO: GO:0004861; F:cyclin-dependent protein kinase inhibitor a. . . ; IEA.  
GO: GO:0016301; F:kinase activity; IEA.  
GO: GO:0007050; P:cell cycle arrest; IEA.  
InterPro: IPR003175; CDI.  
Pfam: PF02234; CDI; 1.  
Cyclin; Kinase.  
SEQUENCE 286 AA; 31719 MW; 1CEBA72583302AAD CRC64;

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Query Match      16.5%; Score 172; DB 2; Length 286;
Best Local Similarity 23.7%; Pred. NO. 0.0021;
Matches 57; Conservative 44; Mismatches 80; Indels 60; Gaps 9;

1 PRDLP-----KNPREKMSERKRELAEBASS-----TSPFLKTKL 37
  ||| ||| ||| :|:|: | | | | | | | | | | | | | | | | | |
71 PSLPPTASPNPPSKQMKKKQQQNDCCGYLQLSRRLQKQPIIIVIRSTRRKQQR 130
  ||| ||| ||| :|:|: | | | | | | | | | | | | | | | | | |
38 NDDSSDPDSDHVIQVAVSSSVASSAALASDECSTVIGGEESDQSSSISSGCTSESKE 97
  ||| ||| ||| :|:|: | | | | | | | | | | | | | | | | | |
131 NETCGRNPNRS-----NLDSTRGDSRSDSVSVFQKKDLISEIN----- 174
  ||| ||| ||| :|:|: | | | | | | | | | | | | | | | | | |
98 IAKNSSSFG---VDLEDHQIETETSTFTITSFRKE--TSPVSEG-----LGETTME 147
  ||| ||| ||| :|:|: | | | | | | | | | | | | | | | | | |
175 ---KPTFGQNFDEEEHTQTRTRESTPCSLRRRPEIMTTPGSSIKINICVSESQRED 231
  ||| ||| ||| :|:|: | | | | | | | | | | | | | | | | | |
148 SSSATKRKGQVRYKTPTAABIEDFLGELSPPDKKKQFIKYNFDIVNDPLEGRYKWD 207
  ||| ||| ||| :|:|: | | | | | | | | | | | | | | | | | |
232 SLRSRHRRR-----PTTPEMDEFFSGAE--EQQQKFIKYNFDVPWNEQLPGRFEWTK 283
  ||| ||| ||| :|:|: | | | | | | | | | | | | | | | | | |

208 L 208
:
284 V 284
Db

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RESULT 13
Q6T223 PRELIMINARY; PRT; 205 AA.
Q6T223;
Q6T223;
Q6T223;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Cyclin-dependent kinase inhibitor 1;1.
Glycine max (Soybean).
OS
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosid1 I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
NCBI_TaxID=3847;
[1]
SEQUENCE FROM N.A.
Li S., Reverdatto S., Nielsen N.C.;
Submitted (Oct-2003) to the EMBL/GenBank/DBJ databases.
EMBL; AY439101; AAS13374.1; -.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. . .; IEA.
GO; GO:0016301; F:kinase activity; IEA.
GO; GO:0007050; P:cell cycle arrest; IEA.
InterPro: IPR003175; CDI.
Pfam: PF02234; CDI; 1.
Cyclin; Kinase.
SEQUENCE 205 AA; 22875 MW; 1B6F2D481710205E CRC64;
(SQ

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Query Match 16.2%; Score 169; DB 2; Length 205;  
Best Local Similarity 30.2%; Pred.No. 0.0022;  
Matches 61; Conservative 33; Mismatches 82; Indels 26; Gaps 9;

OY 20 LAEEASSTFSPFLKTKYLNDSDDSDSHDIVFAVSSSVASSAALADECSVTIGGEE 79  
||| : : : : : ||| : : :  
: : : : : : : : :

```

Db      15  LAMEAVSSABPSSKRRKKIENSTNQEPKLSKTP--RTSSSSAVKPAVTWVRPVSS----- 67
Qy      80  SDQSSGISGCFSTSEKEI-----AKNSSSFGVD-----LEDHOIET-ETETSTFITSN-- 127
Db      68  ---PEWVQOECLSPTSEIPASCCSSNGSIGLDQDRIKLLDLEVASQAVETSTCNGGHEI 124
Qy     128  FRKETGVSGLGETTTEMESSATKRKQGVKRT-PTAAETEDLFSLESPDDKKKQFT 186
Db     125  ERREMKRSSE-LRENSQPEPEMEINSHRVLSKAKAMPTLELEPEPFAASEK--DIQKRQF 181
Qy     187  EKNFDIVNDEPLEGRYKWDRL 208
Db     182  DRYNDIVKQVPLEGRYEWQL 203

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RESULT 14	
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ID	O48597
AC	O48597; (T-EMBLrel. 06, Created)
DT	01-JUN-1998 (T-EMBLrel. 06, Last sequence update)
DT	01-JUN-1998 (T-EMBLrel. 06, Last sequence update)
DT	01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE	Cyclin-dependent kinase inhibitor protein.
DE	Cyclin-dependent kinase inhibitor protein.
GN	Name=CDK11;
OS	Chenopodium rubrum (Red goosefoot) (Pigweed).
OS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC	Caryophyllales; Amaranthaceae; Chenopodium.
NCBI_TaxID=3560;	
NCBI_TaxID=3560;	
[1]	
SEQUENCE FROM N.A.	
RP	MEDLINE=99329903; PubMed=10409053;
RP	Fountain M.D., Renz A., Beck E.;
RA	"Isolation of a cDNA encoding a G1-cyclin-dependent kinase inhibitor
RT	from suspension-cultured photoautotrophic chenopodium rubrum cells.";
RT	Plant Physiol. 120:339-359 (1999).
RL	EMBL; AJ002173; CRA05215.1; -.
RL	PIR; T09968; T09968.
DR	GO; GO:0005634; C:nucleus; IEA.
DR	GO; GO:0004861; F:cyclin-dependent protein kinase inhibitor a. . . ; IEA.
DR	GO; GO:0016301; F:kinase activity; IEA.
DR	GO; GO:0007050; P:cell cycle arrest; IEA.
DR	InterPro; IPR003175; CDI.
DR	Pfam; PF02234; CDI; 1.
DR	Cyclin; Kinase.
SO	SEQUENCE 196 AA; 21685 MW; 150349F7ED82A6B2 CRC64;

Query Match	16.1%;	Score 168.5;	DB 2;	Length 196;	
Best Local Similarity	27.0%;	Pred. No. 0.0023;			
Matches	60;	Conservative 32;	Mismatches 63;	Indels 67;	Gaps 10;
Qy	20	LAEAGSTSPKTKLNDSSD-----SSPDSDVIVFAVSSSSSVASSAAL	66		
Db	1	MAAAAPTS-SPAKKIKKYSKSYNPQLRSRKNLSAPEN-----FAELETTPLEVAAV	54		
Qy	67	ASDE----CSVT--IGGESDQSSSSGCF---TSEKIEIAKNSSSFGVDLEDHOIETE	117		
Db	55	VEEEVANCSSSEVITARSDFPPSCSNYDQLSSSEPEVVKDDGLGNRTADPEVES-	113		
Qy	118	TEISTFTISNFRKETSPVSEGLGETTTEMESSATKRQO-----PGVRKT-----P	163		
Db	114	-----GEASKQESURTEAREATKLDODDYATKATKTVQIKMP	151		
Qy	164	TAABIEDLFESESPDKKQKOFTEKNFNDIVNDEPLEGRYKW	205		
Db	152	SDSEIEFFFAVK--DLQRFSEKNFNDIVKDVPLKGRYDW	191		

RESULT 15	
Q8GVJ3	
ID Q8GVJ3	PRELIMINARY;
AC Q8GVJ3	PRT; 286 AA.
DT 01-MAR-2003	TREMBLrel. 23, Created)

Search completed: September 30, 2005, 11:35:34  
Job time : 89 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 30, 2005, 09:05:51 ; Search time 3087 Seconds  
(without alignments)  
9826.033 Million cell updates/sec

Title: US-09-980-758A-7  
Perfect score: 626  
Sequence: 1 ctccgagattaccacaaat.....acaagtggagtcgactttaaa 626

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.\*

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- 2: gb\_hgt.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sta.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	626	100.0	626	6	BD267733 Method of
2	612.8	97.9	824	6	AX008797 Sequence
3	612.8	97.9	824	6	AX463066 Sequence
4	611.4	97.7	840	8	AF106705 Arabidops
5	589.4	94.2	591	8	AJ301557 Arabidops
6	335.8	53.6	81875	8	AF000419 Arabidops
7	204.4	32.7	4116	8	AF208692 Arabidops
8	122	19.5	588	8	AJ301558 Arabidops
9	122	19.5	642	6	AX008798 Sequence
10	122	19.5	642	6	AX463067 Sequence
11	58	9.3	7218	6	I66494 Sequence 14
12	53	8.5	927	8	AB029483 Pisum sat
13	49.6	7.9	597	8	AY439102 Glycine m
14	47.2	7.5	618	8	AY439101 Glycine m
15	46.6	7.4	104679	8	AC011807 Arabidops
16	46.4	7.4	499	8	AY439104 Glycine m
17	46.2	7.4	804	6	AX008805 Sequence
18	46.2	7.4	804	6	AX463073 Sequence
19	46.2	7.4	804	8	AJ002173 Chenopodi

20	45.8	7.3	377	6	AX008795 Sequence
21	45.8	7.3	377	6	AX463063 Sequence
22	45.8	7.3	443	6	AX008794 Sequence
23	45.8	7.3	443	6	AX463064 Sequence
24	45.8	7.3	660	6	AX008793 Sequence
25	45.8	7.3	660	6	AX463062 Sequence
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31	45	7.2	225203	2	AC124569 Mus muscu
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36	44.6	7.1	1341	8	AY087958 Arabidops
37	44.6	7.1	184458	2	AC141779 Apis mell
38	43.6	7.0	1312	8	AK117586 Arabidops
39	43.6	7.0	202882	10	AC139568 Mus muscu
40	43.4	6.9	1072	8	NTA517189 Nicotiana
41	43	6.9	533	6	AX008799 Sequence
42	43	6.9	533	6	AX463068 Sequence
43	43	6.9	669	6	CQ803834 Sequence
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## ALIGNMENTS

RESULT 1  
BD267733

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BD267733 626 bp DNA linear PAT 17-JUL-2003  
Method of promoting plant cell proliferation by functionally  
inhibiting plant cyclin inhibitor gene.

BD267733 1 GI:33077501

JP 2002543823-A/4.

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 626)

Roberts, J. and Kelly, B.

Method of promoting plant cell proliferation by functionally

inhibiting plant cyclin inhibitor gene

Patent: JP 2002543823-A 4 24-DEC-2002;

PRED HUTCHINSON CANCER RESEARCH CENTER

OS Arabidopsis thaliana (thale cress)

PN JP 2002543823-A/4

PD 24-DEC-2002

PF 15-MAY-2000 JP 2000618299

PI 14-MAY-1999 US 60/134373

PC JAMES ROBERTS, BETH KELLY

promoting plant cell proliferation by functionally CC

inhibiting

CC plant cyclin inhibitor gene

FH Key Location/Qualifiers

FT source 1..626

FT /organism='Arabidopsis thaliana (thale

cress)';

Location/Qualifiers

1..626

/organism='Arabidopsis thaliana'

/mol\_type='Genomic DNA'

/db\_xref='taxon:3702'

FEATURES

source

ORIGIN

Query Match 100.0%; Score 626; DB 6; Length 626;

Best Local Similarity 100.0%; Pred. No. 5.8e-169;

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QY 601 GTCGCTACAAGTGGGATCGACTTTAA 626
Db 601 GTCGCTACAAGTGGGATCGACTTTAA 626
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RESULT 2
AX008797
LOCUS AX008797 824 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 7 from Patent WO9964599.
ACCESSION AX008797
VERSION AX008797.1 GI:9996261
KEYWORDS
SOURCE
ORGANISM
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
REFERENCE
AUTHORS Powke,L.C., Wang,H. and Crosby,W.I.
TITLE Cyclin-dependent kinase inhibitors as plant growth regulators
JOURNAL Patent: WO 9964599-A 7 16-DEC-1999;
FOWKE LARRY C (CA); WANG HONG (CA); AGRICULTURE AND AGRIFOOD CANAD
(CA); CANADA NAT RES COUNCIL (CA); CROSBY WILLIAM L (CA); UNIV
SASKATCHEWAN TECHNOLOGIES (CA)
FEATURES
Location/Qualifiers
1..824
source
/organism="Arabidopsis thaliana"
/mol_type="unassigned DNA"
/db_xref="taxon:3702"
ORIGIN
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Query Match 97.9%; Score 612.8; DB 6; Length 824;
Best Local Similarity 99.7%; Pred. No. 3.7e-165;
Matches 614; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 11 ACCCAAAATCCAGAGAGAAAAAATGAGCGAGAGAAAGCGAGAGCTTGAGAGAAGC 70
Db 24 ACACAAAATCCAGAGAGAAAAAATGAGCGAGAGAAAGCGAGAGCTTGAGAGAAGC 83
QY 71 TTCAGCACAAGCTTCTCACCACCTGAAGAAACGAAGCTTAAATGATCTTCTGATTTCATC 130
Db 84 TTCAGCACAAGCTTCTCACCACCTGAAGAAACGAAGCTTAAATGATCTTCTGATTTCATC 143
QY 131 ACCGAGCTCTCATGACGTCATCGTCTTCGCGGTTTCATCTTCTCCGTTGCTTCGTCGCG 190
Db 144 ACCGAGCTCTCATGACGTCATCGTCTTCGCGGTTTCATCTTCTTCGTTGCTTCGTCGCG 203
QY 191 GCGTTAGCGTCTGATGAATGTTCCGTTACCATCGTGGAGAAAGTGAATGATCAGTCCTC 250
Db 204 GCGTTAGCGTCTGATGAATGTTCCGTTACCATCGTGGAGAAAGTGAATGATCAGTCCTC 263
QY 251 GAGTATCAGCTCCGTTGTTTCCACGAGTGAATCGAAAGAAATCGCGAAGAAACAGTTCGTC 310
Db 264 GAGTATCAGCTCCGTTGTTTCCACGAGTGAATCGAAAGAAATCGCGAAGAAACAGTTCGTC 323
QY 311 GTTTGGTGTAGATCTGGAGGATCATCAATCGAAACCGAAACCGAAACCTCAACATTCAT 370
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QY 611 GTGGGATCGACTTTAA 626
Db 624 GTGGGATCGACTTTAA 639
RESULT 3
AX463066
LOCUS AX463066 824 bp DNA linear PAT 15-JUL-2002
DEFINITION Sequence 7 from Patent WO0250292.
ACCESSION AX463066
VERSION AX463066.1 GI:21886079
KEYWORDS
SOURCE
ORGANISM
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
REFERENCE
AUTHORS Powke,L.C., Wang,H. and Zhou,Y.
TITLE Modulation of plant cyclin-dependent kinase inhibitor activity
JOURNAL Patent: WO 0250292-A 7 27-JUN-2002;
University of Saskatchewan Technologies (CA); Minister of
Agriculture and Agrifood Canada (CA)
FEATURES
Location/Qualifiers
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ORIGIN
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## ORIGIN

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Best Local Similarity	99.8%;	Pred. No. 9.Se-165;		
Matches 612;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
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RESULT 5
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LOCUS
DEFINITION
Arabidopsis thaliana mRNA for cyclin-dependent kinase inhibitor 6
(krp6 gene).
ACCESSION
AJ301557
VERSION
AJ301557.1 GI:14422294
KEYWORDS
cyclin-dependent kinase inhibitor; krp6 gene.
SOURCE
Arabidopsis thaliana
ORGANISM
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
De Veylder, L., Beeckman, T., Beeckman, G. T., Krols, L., Terras, P.,
Landrieu, I., van der Schueren, E., Maes, S., Naudts, M., and Inze, D.
Functional analysis of cyclin-dependent kinase inhibitors of
Arabidopsis
Plant Cell 13 (7), 1653-1668 (2001)
21342510
PUBMED
11449057
2 (bases 1 to 591)
De Veylder, L.
Direct Submission
Submitted (31-OCT-2000) De Veylder L., Departement Plantegenetica,
Vlaams Interuniversitair Instituut voor Biologie (VIB), K.L.
Ledeganckstraat 35, B-9000 Gent, BELGIUM
Location/Qualifiers
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ORIGIN
Query Match
Best Local Similarity 99.8%; Score 589.4; DB 8; Length 591;
Matches 590; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 36 ATGAGCGAGAGAAAGCGAGGTTGCAGAAAGCTTCAAGCACAAAGCTTTCACCACTG 95
Db 1 ATGAGCGAGAGAAAGCGAGGTTGCAGAAAGCTTCAAGCACAAAGCTTTCACCACTG 60
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Db 61 AAGAAAAACGAAGCTTAATGATCTTCTGATTCATCACCAGGATCTCTGATGATCGTC 120
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Db 181 GTTACCATCGTGGAGAAAGATGATCAGTCTCTGAGTATCAGTCCGGTTGTTTCACC 240
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RESULT 6
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LOCUS
DEFINITION
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ACCESSION
AP000419 BA000014
VERSION
AP000419.1 GI:5832740
KEYWORDS
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
Kaneko, T., Katoh, T., Sato, S., Nakamura, A., Asamizu, E. and Tabata, S.
Structural analysis of Arabidopsis thaliana chromosome 3. II.
Sequence features of the 4,251,695 bp regions covered by 90 P1, TAC
and BAC clones
DNA Res. 7 (3), 217-221 (2000)
20363099
PUBMED
10907853
2 (bases 1 to 81875)
Kaneko, T., Katoh, T., Sato, S., Nakamura, Y., Asamizu, E. and Tabata, S.
Direct Submission
Submitted (03-SEP-1999) Yasukazu Nakamura, Kazusa DNA Research
Institute, Department of Plant Gene Research; 1532-3, Yana,
Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp,
Tel:81-438-52-3935, Fax:81-438-52-3934)
Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MW11
Genes with similarity to proteins in the databases are described in
'product' or 'note' qualifiers. Genes that have no significant
protein similarity are described as 'unknown protein'.
The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/Grail-1.3/),
GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
NetGene2 (S.W. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
SplicePredictor (Volker Brendel, Stanford University,
http://gremli1.zool.iastate.edu/cgi-bin/sp.cgi).
Genes encoding tRNAs are predicted by tRNAscan-SE
(Sean Eddy, Washington University School of Medicine, St. Louis,
http://genome.wustl.edu/eddy/tRNAscan-SE/).
This sequence may not be the entire insert of this clone. It may be
shorter because we remove overlaps between neighboring submissions.
The 5' clone is MHP21 and the 3' clone is MLD14.
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Query Match 53.6%; Score 335.8; DB 8; Length 81875;

Best Local Similarity 73.7%; Pred. No. 2.8e-85;

Matches 552; Conservative 0; Mismatches 2; Indels 195; Gaps 2;

QY	11	ACCCAAATCCAGAGAGAAAAAATGACGAGAGAAAGCAGAGCTTGCGAGAGAGC	70
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RESULT 7

AF208692

LOCUS

DEFINITION Arabidopsis thaliana 4116 bp DNA linear PLN 30-NOV-2001

AF208692 Arabidopsis thaliana cyclin-dependent kinase inhibitor p22ack1

AF208692 (ACK1) gene, promoter region and partial cds.

ACCESSION AF208692

VERSION AF208692.1 GI:17154784

KEYWORDS Arabidopsis thaliana (thale cress)

SOURCE Arabidopsis thaliana

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsiis.  
1 (bases 1 to 4116)  
Cho,J.W. and Park,S.C.

Cell cycle control study in plant: control of plant growth and  
development by G1 specific cyclin D1 and a novel D1 specific cyclin  
dependent kinase inhibitor, p22ack1

REFERENCE

TITLE

JOURNAL

Unpublished

2 (bases 1 to 4116)

Cho,J.W. and Park,S.C.

Direct Submission

Submitted (28-NOV-1999)

Plant Growth and Development, Kumho Life &

Environmental Science Laboratory, 1 Oryongdong Bukku, Kwangju

500-712, Korea

Location/Qualifiers

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Matches 205; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 3911 ACACAAAATCCAGAGAGAAAAAATGACGAGAGAAAGCAGAGCTTGCGAGAGAGC

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QY 191 GGCTTTAGCGTCTGATGATGATTCGCG 216

Db 4091 GGCTTTAGCGTCTGATGATGATTCGCG 4116

RESULT 8

ATH301558

LOCUS

DEFINITION Arabidopsis thaliana mRNA for cyclin-dependent kinase inhibitor 7

ATH301558

588 bp mRNA linear PLN 26-JUL-2001

(krp7 gene).

ACCESSION AJ301558

VERSION AJ301558.1 GI:14422296

KEYWORDS cyclin-dependent kinase inhibitor; krp7 gene.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsiis.

REFERENCE

1

AUTHORS	De Veylder, L., Beekman, T., Beemster, G.T., Krols, L., Terras, F., Landrieu, I., van der Schueren, E., Maes, S., Naudts, M. and Inze, D.
TITLE	Functional analysis of cyclin-dependent kinase inhibitors of Arabidopsis
JOURNAL	Plant Cell 13 (7), 1653-1668 (2001)
MEDLINE	21342510
PUBMED	11443057
REFERENCE	2 (bases 1 to 588)
AUTHORS	De Veylder, L.
TITLE	Direct Submission
JOURNAL	Submitted (31-OCT-2000) De Veylder L., Departement Plantegenetica, Vlaams Interuniversitair Instituut voor Biologie (VIB), K.U.L. Ledeganckstraat 35, B-9000 Gent, BELGIUM
FEATURES	<p>Location/Qualifiers</p> <p>1..588</p> <p>/organism="Arabidopsis thaliana"</p> <p>/mol_type="mRNA"</p> <p>/db_xref="taxon:3702"</p> <p>1..588</p> <p>/gene="krp7"</p> <p>1..588</p> <p>/gene="krp7"</p> <p>/function="cell cycle control"</p> <p>/codon_start=1</p> <p>/product="cyclin-dependent kinase inhibitor 7"</p> <p>/protein_id="CAC41621.1"</p> <p>/db_xref="GI:14422297"</p> <p>/db_xref="GOA:Q94CL9"</p> <p>/db_xref="UniProt/T/EMBL:Q94CL9"</p> <p>/translation="MSTETKPKRSEYEGSNIKMRLLLLDDDDVLRSPRTLSSSSSSSLSI  AYSVSGFCVSALLSEEDHRRSSISSGSSSTNEIATRIUFPFSDLEAHEISETI  STLLTNFRQGSVSSNLGETAEMDSATTEMRDQRTEKKKMEKSPTOAELDDFFS  AABRYEQKRFTEKYNIDVINDTPLEGRYQWVSLKP"</p>
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Best Local Similarity	63.0%; Pred. No. le-23;
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Db	177 ATCTGAAGAAGAGACCATCATCGAAGCTCAAGCATCAGCTCTGTTGTTCCAGCAGCA 236
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Db	465 TGATGACTTTTCTCGCGCGCGGAGAG-----ATACGAAACAGAAACGATTCACAGAAAA 518
QY	563 GTACAACTTCGATATTGTCATGACGAAACCGCTTTGAAGTTCGCTACAGTGGGATCGACT 622
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QY	623 TTAAT 626

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DEFINITION Sequence 8 from Patent WO0250292.
ACCESSION AX463067
VERSION AX463067.1 GI:21886080
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
REFERENCE 1
AUTHORS Powke,L.C., Wang,H. and Zhou,Y.
TITLE Modulation of plant cyclin-dependent kinase inhibitor activity
JOURNAL Patent: WO 0250292-A 8 27-JUN-2002;
University of Saskatchewan Technologies (CA); Minister of
Agriculture and Agrifood Canada (CA)
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QY 615 GAAA 618
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RESULT 11
LOCUS I66494/c
DEFINITION Sequence 14 from patent US 5670367.
ACCESSION I66494
VERSION I66494.1 GI:2724471
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
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REFERENCE 1 (bases 1 to 7218)
AUTHORS Dörner,F., Scheiflinger,F. and Falkner,F.Gunter.
TITLE Recombinant fowlpox virus
JOURNAL Patent: US 5670367-A 14 23-SEP-1997;
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Matches 4; Conservative 215; Mismatches 125; Indels 0; Gaps 0;
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LOCUS AB029483
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complete cds.
ACCESSION AB029483
VERSION AB029483.1 GI:12081914
KEYWORDS cyclin dependent kinase inhibitor.
SOURCE P15um sativum (pea)
ORGANISM P15um sativum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae;
Pisum.
REFERENCE 1 (bases 1 to 927)
AUTHORS Shimizu-Sato,S. and Mori,H.
TITLE A cDNA from Pisum sativum encoding the cyclin-dependent kinase
inhibitor (CKI) homologue
JOURNAL Published Only in DataBase (2001)
REFERENCE 2 (bases 1 to 927)
AUTHORS Shimizu-Sato,S. and Mori,H.
TITLE Direct Submission
JOURNAL Submitted (01-JUL-1999) Sae Shimizu-Sato, Nagoya University,
Graduate School of Bioagricultural Sciences; Chikusa, Nagoya, Aichi
464-8601, Japan (E-mail:saesagr.nagoya-u.ac.jp,
Tel:+81-52-789-4166, Fax:+81-52-789-4296)
Location/Qualifiers
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QY 600 GGTCTGCTACAAGTGGGATC 618
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DEFINITION cds.
ACCESSION AY439102 GI:46844157
VERSION AY439102.1
KEYWORDS Glycine max (soybean)
SOURCE Glycine max
ORGANISM Glycine max (soybean)
REFERENCE 1 (bases 1 to 597)
AUTHORS Li, S., Reverdatto, S. and Nielsen, N.C.
TITLE cDNA of cell-cycle genes in soybean cotyledons
JOURNAL Unpublished
AUTHORS Li, S., Reverdatto, S. and Nielsen, N.C.
TITLE Direct Submission
JOURNAL Submitted (16-OCT-2003) ARS-USDA, Agronomy, Purdue University, 1150 Lilly Hall of Life Sciences, West Lafayette, IN 47906-1150, USA

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DEFINITION cds.
ACCESSION AY439101 GI:42362357
VERSION AY439101.1
KEYWORDS Glycine max (soybean)
SOURCE Glycine max
ORGANISM Glycine max (soybean)
REFERENCE 1 (bases 1 to 618)
AUTHORS Li, S., Reverdatto, S. and Nielsen, N.C.
TITLE cDNA of cell-cycle genes in soybean cotyledons
JOURNAL Unpublished
AUTHORS Li, S., Reverdatto, S. and Nielsen, N.C.
TITLE Direct Submission
JOURNAL Submitted (16-OCT-2003) ARS-USDA, Agronomy, Purdue University, 1150 Lilly Hall of Life Sciences, West Lafayette, IN 47906-1150, USA

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QY 595 TTGAAGGTCGCTACAAAGTGGGATC 618
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Db 581 TGGAAGGACGCTACGAGTGGGTTT 604
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DEFINITION complete sequence.
ACCESSION AC011807 GI:6693374
VERSION AC011807.4
KEYWORDS HTG.
SOURCE Arabidopsis thaliana (chale cress)
ORGANISM Arabidopsis thaliana
REFERENCE 1 (bases 1 to 104679)
AUTHORS Arabidopsis thaliana
TITLE Arabidopsis thaliana
JOURNAL Submitted (16-OCT-2003) ARS-USDA, Agronomy, Purdue University, 1150 Lilly Hall of Life Sciences, West Lafayette, IN 47906-1150, USA

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Query Match 7.9%; Score 49.6; DB 8; Length 597;
Best Local Similarity 72.7%; Pred. No. 0.0074;
Matches 64; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

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Db 560 TGGAAGGACGCTACGAGTGGGTTCAATT 587
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RESULT 14
AY439101 618 bp mRNA linear PLN 01-MAY-2004
LOCUS Glycine max cyclin-dependent kinase inhibitor 1;1 mRNA, complete
DEFINITION cds.
ACCESSION AY439101 GI:42362357
VERSION AY439101.1
KEYWORDS Glycine max (soybean)
SOURCE Glycine max
ORGANISM Glycine max (soybean)
REFERENCE 1 (bases 1 to 618)
AUTHORS Li, S., Reverdatto, S. and Nielsen, N.C.
TITLE cDNA of cell-cycle genes in soybean cotyledons
JOURNAL Unpublished
AUTHORS Li, S., Reverdatto, S. and Nielsen, N.C.
TITLE Direct Submission
JOURNAL Submitted (16-OCT-2003) ARS-USDA, Agronomy, Purdue University, 1150 Lilly Hall of Life Sciences, West Lafayette, IN 47906-1150, USA

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ORIGIN
Query Match 7.5%; Score 47.2; DB 8; Length 618;
Best Local Similarity 72.6%; Pred. No. 0.036;
Matches 61; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

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QY 595 TTGAAGGTCGCTACAAAGTGGGATC 618
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Db 581 TGGAAGGACGCTACGAGTGGGTTT 604
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RESULT 15
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LOCUS Arabidopsis thaliana chromosome I BAC F14J22 genomic sequence, complete sequence.
DEFINITION complete sequence.
ACCESSION AC011807 GI:6693374
VERSION AC011807.4
KEYWORDS HTG.
SOURCE Arabidopsis thaliana (chale cress)
ORGANISM Arabidopsis thaliana
REFERENCE 1 (bases 1 to 104679)
AUTHORS Arabidopsis thaliana
TITLE Arabidopsis thaliana
JOURNAL Submitted (16-OCT-2003) ARS-USDA, Agronomy, Purdue University, 1150 Lilly Hall of Life Sciences, West Lafayette, IN 47906-1150, USA

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ORIGIN
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Best Local Similarity 72.7%; Pred. No. 0.0074;
Matches 64; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

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|||||
Db 521 AAGACATTCAGAAACGATTTCAAGACAGATACATATGATATTGTTAAGGACGTACCGC 580
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```

REFERENCE AUTHORS	1 (bases 1 to 104679) Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Araujo,R., Huizar,L., Rowley,D., Buehler,E., Dunn,P., Gonzalez,A., Kremenetskaia,I., Kim,C., Lenz,C., Li,J., Liu,S., Luros,S., Schwartz,J., Shinn,P., Toriumi,M., Vyotskaia,V.S., Walker,M., Yu.G., Ecker,J., Theologis,A. and Davis,R.W. Unpublished
JOURNAL REFERENCE AUTHORS	2 (bases 1 to 104679) Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Nguyen,M., Lam,B., Southwick,A., Bei,Q., Buehler,E., Chin,C., Chiou,J., Choi,E., Dunn,P., Gonzalez,A., Howng,B., Kim,C., Koo,T., Lee,J.M., Lenz,C., Li,J., Liu,A., Liu,K., Li,J., Liu,S., Mukharkey,N., Phan,P., Sakano,H., Schwartz,J., Shinn,P., Thaveri,A., Toriumi,M., Vaysberg,M., Walker,M., Yu.G., Ecker,J., Theologis,A. and Davis,R.W. Direct Submission
TITLE JOURNAL	Direct Submission Submitted (15-OCT-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA
REFERENCE AUTHORS	3 (bases 1 to 104679) Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Araujo,R., Huizar,L., Rowley,D., Buehler,E., Dunn,P., Gonzalez,A., Kremenetskaia,I., Kim,C., Lenz,C., Li,J., Liu,S., Luros,S., Schwartz,J., Shinn,P., Toriumi,M., Vyotskaia,V., Walker,M., Yu.G., Ecker,J., Theologis,A. and Davis,R.W. Direct Submission
TITLE JOURNAL	Direct Submission Submitted (14-JAN-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA
REFERENCE AUTHORS	4 (bases 1 to 104679) Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Nguyen,M., Lam,B., Southwick,A., Ecker,J., Theologis,A. and Davis,R.W. Direct Submission
TITLE JOURNAL	Direct Submission Submitted (13-SEP-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA
COMMENT	On Jan 14, 2000 this sequence version replaced gi:6692246. Bases 92948-104679 of IGF clone F14J22 overlap with bases 1-11732 of IGF clone F13r21 (gb AC007504). e-mail for correspondence: arabesque@stanford.edu Genes with similarity to proteins in the databases are named 'putative', '-like' or 'similar to'. Genes that have EST similarity but no significant protein similarity are described as 'unknown proteins'. Genes that are annotated based only on gene prediction software are described as 'hypothetical proteins'. The gene prediction programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://combio.ornl.gov/section/index.html), GENSCAN (Chris Burge, http://genes.mit.edu/GENSCAN.), FEXA (Victor Solovyev, http://genomic.sanger.ac.uk/gf/gf.shtml), and NetPlantGene (S.M. Hebagaard, et al., CBS, Technical University of Denmark,http://www.cbs.dtu.dk/NetPlantGene.html). Location/Qualifiers 1. .104679 /organism="Arabidopsis thaliana" /mol_type="genomic DNA" /db_xref="taxon:3702" /chromosome="I" /clone="F14J22" 6567. .7832 /gene="F14J22.1" 6567. .7832 /gene="F14J22.1" /codon_start=1 /product="Hypothetical protein" /protein_id="AAG13057.1" /db_xref="GI:10120432" /translation="MPGNLEPLDGIQIPYHFRCPISIDLMSDPVTISTGOTYDRTSI DSWIANGNTCPVTFVALSDFTLIPNHTLRLIQEWCVANRSGVERIPTKQADPI SVRLLSASAITGTHSVSRRAAIRLRGLARSEKNRVLIIGNAREILVRILFA DIETVLSLSVESLALLVLLHMTETECEAVADPSRPGWFTMLLPDSSIEIRVNA ALIEMVLTKAASMDLKLITISGSDSIFEGVLDDLKNPISRRAALKIGIKAI FALCLIVK
FEATURES source	TRHLAISAGAPGILIDRLAADFDRCDTERGLATVELLCRLPEGCAAFGEHALTVPLMV XTILRVSDRATEYAGALLALCTAEERCDEAAAAGLVQTQLLLVQSDCTERAKKAQ MLLILRDSWDDSTVHSDDDNRSEVPF" complement (10438. .12278) /gene="F14J22.2" complement (join (10438. .11034,11973. .12278)) /gene="F14J22.2" /codon_start=1 /evidence=not_experimental /product="Hypothetical protein" /protein_id="AAG13058.1" /db_xref="GI:10120433" /translation="MTNAQLGQGFWMGINSDDSGGCKRIEKPELPSPHSHPSE IQTTVTKGKRTKRNKNHEESPDEIHIWTRERREKMRDMFSLKHALLPOLPPK ADKSTIVDEAVSSIKSLEQTLKLEMQKLEKLOYSSASTNTPTTTPAYASSSSSPT ALLTISNHPIDATDTSIPRAAFADQVSSSAAANLPYCNDPIVNFDTWSRNV VLITCGNEAFFNLCVPKHKGFVFTSCVLYLFKYNNEVLFAVNSNVFVSTVIQAVS YTYNHFYHMICGDIYILPWFPPFM" complement (17103. .20116) /gene="F14J22.3" complement (join (17103. .17345,17435. .17638,17727. .17921, 17999. .18133,18225. .18314,18416. .18493,18579. .19235, 19372. .19490,19822. .20116)) /gene="F14J22.3" /codon_start=1 /evidence=not_experimental /product="Putative Poly-A Binding Protein" /protein_id="AAG13056.1" /db_xref="GI:10120431" /translation="MAQIQHQNGNAVPGAAAAFAAAAAAGAAAAAGAAQOQT TSLYVGLDQVTSQLEAFQAGQVSVRCRDMTTRSLGIGYVNYATPQDASRA LNEINFALNGRAIRVMYSVRDPSLRKSGVNI FIKLNDKSIDHAKHETSAFGPIL SCKYAVDPSGQSGYGFQVYDTDEAQAQIDKLGMLLNDKQVYVPPVHKLRDPSG EKVFTNIVYVKNLSSESDELNKVGFEGVTTCVIMRDGEGSKGFGVNFENSD AARAVDALNGKTFDDKEMFQAQKQKSERETELKQKESLKEADSKSGSNLYVKNL DESYTDKLRHEFAFGTITSCVMRDPGVSRSRGVFAFSTPEEATRAITEMNGKI VTKPLYVALAQRKDRKARLQAQFQMRPVNMPVAVGMOMYPPGPGPMQQLFYQG GPPAMI PQGFGYQQLVPGMRPGSPMPNPFMPMQOQQOQQOQQOQQOQQOQQOQQO ALPOQPSPMWQQQMHGEMRYVRQDYNVTMEGPTQNMLSVRYDYSVSSGGVHRRG LTPQSPFIVALLATRIANAPEQQRTMLGENLYPLVEQLEPESAAKVTGMLLEMDQTEV LHLLSEPEALKAKVTEAMDVLRSVAQQQAAGADQLASLSLGDNIVP" 24077. .25793 /gene="F14J22.4" join (24077. .24984,25103. .25793) /gene="F14J22.4" /evidence=not_experimental /protein_id="AAG13059.1" /db_xref="GI:10120434" /translation="MASILSILLILSLNLSNLTSTTGNHINDRKLSLEIITGGNDN NPPSPSPPEPEPADCPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP PAPPKQPSPTDLPFLFASLLKKVYVLRQKDLVADDKLSWEGPDICNKLGLCK AI RPKTKHALASVQFQNLGRKIGIKLIDNFDLKEVTI PHANSNGTGSVPDF SNKLXYELDLNNKLTGDPTSVLKGNNLTFLDRFNSFSGSVPPQVFNLDLVLFI NNNLVOKLPLNGLITALLYITFANNRFTGIPESIGNIKYQLQVLEFNLNKLTCGLPI QIGNLTRATVDFVGNLTGPIPYSGFQLETMQNLGNKRFYGTIPEIVCEIACLQN VLSNNYFTQVQPKRKLIRKIMDVSMNCILDLNOKTPECAKFFMRKQTCPSKS LFTVPCDNPNRGKPDQERLEEKAAQVSHPVYNTLNPDRLRNL" complement (27081. .29147) /gene="F14J22.5" complement (join (27081. .27408,27492. .27578,27658. .27881, 27973. .28276,28385. .28483,28564. .28824,29045. .29147)) /gene="F14J22.5" complement (join (27388. .27408,27492. .27578,27658. .27881, 27973. .28276,28385. .28483,28564. .28824,29045. .29138)) /gene="F14J22.5" /note="Unknown protein" /codon_start=1 /evidence=not_experimental



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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 30, 2005, 09:05:47 ; Search time 476 Seconds  
(without alignments)  
7785.206 Million cell updates/sec

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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  - 2: Geneseqn1990s:\*
  - 3: Geneseqn2000s:\*
  - 4: Geneseqn2001as:\*
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  - 9: Geneseqn2003bs:\*
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  - 12: Geneseqn2004as:\*
  - 13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	612.8	97.9	824	3 AAZ29417	Aaz29417 Arabidops
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6	52	8.3	467	3 AAA95291	Aaa95291 Soybean c
7	48.8	7.8	424	3 AAN02392	Aan02392 Soybean c
8	48.8	7.8	424	3 AAA95278	Aaa95278 Soybean c
9	48.8	7.8	620	3 AAA95287	Aaa95287 Soybean c
10	48.8	7.8	620	3 AAN02401	Aan02401 Cyclin de
11	47.2	7.5	1116	3 AAN02402	Aan02402 Cyclin de
12	47.2	7.5	1116	3 AAA95288	Aaa95288 Soybean c
13	46.2	7.4	804	3 AAZ29420	Aaz29420 Chenopodi
14	46.2	7.4	804	6 AAD40768	Aad40768 Chenopodi
15	45.8	7.3	377	6 AAD40762	Aad40762 Arabidops
16	45.8	7.3	443	6 AAD40763	Aad40763 Arabidops
17	45.8	7.3	779	3 AAC47352	Aac47352 Arabidops
18	45.8	7.3	780	3 AAC36958	Aac36958 Arabidops
19	45.8	7.3	904	3 AAC29415	Aac29415 Arabidops
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	22	44.6	7.1	870	3 AAA95293	Aaa95293 Arabidops
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	24	44.6	7.1	870	12 ADN72346	Adn72346 Thale cre
	25	44.6	7.1	1290	6 AAD40769	Aad40769 Arabidops
	26	44.6	7.1	1341	3 AAC33295	Aac33295 Arabidops
	27	44	7.0	470	3 AAN02403	Aan02403 Cyclin de
	28	44	7.0	470	3 AAA95289	Aaa95289 Soybean c
	29	43	6.9	533	3 AAZ29419	Aaz29419 Arabidops
	30	43	6.9	533	6 AAD40767	Aad40767 Arabidops
	31	43	6.9	669	12 ADN72350	Adn72350 Thale cre
	32	43	6.9	797	6 AAD40771	Aad40771 Arabidops
	33	43	6.9	875	2 AAX25016	Aax25016 Arabidops
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	35	41	6.5	2000	8 ADA71938	Ada71938 Rice gene
	36	40.8	6.5	1193	2 AAX25017	Aax25017 Alfalfa c
	37	39.2	6.3	528	10 ACC60133	Acc60133 Rice endo
	38	38.8	6.2	2355	13 ADS49209	Ads49209 Bacterial
	39	38.2	6.1	3143	2 AAT59504	Aat59504 Candida a
	40	38.2	6.1	3224	2 AAT66688	Aat66688 Candida a
	41	38	6.1	571	5 AAS90731	Aas90731 DNA encod
	42	38	6.1	906	5 AAS88069	Aas88069 DNA encod
	43	38	6.1	906	5 AAS68116	Aas68116 DNA encod
	44	38	6.1	993	5 AAS90706	Aas90706 DNA encod
	45	38	6.1	993	5 AAS68118	Aas68118 DNA encod

## ALIGNMENTS

RESULT 1  
AAC85201  
ID AAC85201 standard; DNA; 626 BP.  
XX  
AC AAC85201;  
XX  
DT 22-MAR-2001 (first entry)  
XX  
DE Plant D-like cyclin inhibitor BRO4 coding sequence.  
XX  
KW Plant; D-like cyclin inhibitor gene; BRO4; hyperplastic; variant;  
KW growth rate; dividing cells; inactivation; protoplast; seed; root cell;  
KW meristem; leaf; ss.  
XX  
OS Arabidopsis thaliana.  
XX  
FH Key Location/Qualifiers  
FT CDS 36..626  
FT /\*tag= a  
FT /product= "BRO4"  
XX  
XX WO200069883-A1.  
XX  
PD 23-NOV-2000.  
XX  
PF 15-MAY-2000; 2000WO-US013379.  
XX  
PR 14-MAY-1999; 99US-0134373P.  
XX  
PA (HUTC-) HUTCHINSON CANCER RES CENT FRED.  
XX  
PI Roberts J, Kelly B;  
XX  
DR WPI; 2001-024998/03.  
XX  
P-PSDB; AAB47001.  
XX  
PT Functionally inactivating expression of plant D-like cyclin inhibitor  
PT gene for producing a hyperplastic variant plant, modulating the growth  
PT and/or yield of plants, and increasing the proportion of dividing cells.  
XX  
PS Claim 16; Page 41; 50pp; English.  
XX  
CC The sequence given in AAC85201 represents a plant D-like cyclin inhibitor

CC gene, BRO4. This sequence may be used to produce a hyperplastic variant  
 CC plant, increase the growth rate of a plant, or increase the proportion of  
 CC dividing cells in a plant cell population, relative to a wild-type plant,  
 CC by functionally inactivating the expression of a plant D-like cyclin  
 CC inhibitor gene in a plant. This sequence is homologous to a sequence  
 CC present in a D-like cyclin inhibitor gene and when integrated at the  
 CC corresponding locus, functionally inactivates plant D-like cyclin  
 CC inhibitor protein expression. BRO4 is useful for producing hyperplastic  
 CC variant plants, increasing the growth rate of a plant and for increasing  
 CC the proportion of dividing cells in a plant cell population comprising  
 CC protoplast, seeds, root cells, meristem cells or leaf cells  
 XX  
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Query Match 100.0%; Score 626; DB 5; Length 626;  
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 DB 301 ACAGTTCGCTGTTGGTGTAGATCTGGAGGATCATCAATCGAAACCGAAACCGAAACCT 360  
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 DB 601 GTCGCTCAAGTGGATCGACTTTAA 626

RESULT 2  
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 ID AAZ29417 standard; cDNA; 824 BP.  
 XX  
 AC AAZ29417;  
 XX  
 DT 29-FEB-2000 (first entry)  
 XX  
 DE Arabidopsis thaliana CDK inhibitor, ICN2 encoding cDNA.  
 XX

KW Cyclin-Dependent kinase inhibitor; CDK; Interactor of Cyclin 2; ICN2;  
 KW Cdc2a; D-class cyclin; CycD1; CycD2; CycD3; morphogenesis;  
 KW antisense construct; tissue-specific promoter; transgenic plant;  
 KW male sterility; ds.  
 XX Unidentified.  
 OS  
 XX  
 FH Key Location/Qualifiers  
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 FT /product= "ICN2"  
 XX  
 PN WO9964599-A1.  
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 PD 16-DEC-1999.  
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 PF 08-JUN-1999; 99WO-CA000532.  
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 PR 31-DEC-1998; 98CA-02256121.  
 XX  
 PA (MIAC ) AGRIC & AGRIFOOD CANADA.  
 PA (UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.  
 PA (CANA ) NAT RES COUNCIL CANADA.  
 XX  
 PI Wang H, Fowke LC, Crosby WL;  
 XX  
 XX WPI: 2000-097540/08.  
 DR P-PSDB; AAY44337.  
 XX  
 XX Modifying plant cell development using nucleic acid encoding inhibitor of  
 PT cyclin-dependent kinase, or corresponding antisense sequence, e.g. for  
 PT inducing male sterility.  
 XX  
 PS Disclosure; Fig 4; 58pp; English.  
 XX  
 CC The present sequence is a cDNA encoding ICN2 which inhibits A. thaliana  
 CC Cyclin-Dependent kinase (CDK). Interactor of Cyclin 2 (ICN2) interacts  
 CC with Cdc2a, D-class cyclins, CycD1, CycD2 and CycD3 and shares functional  
 CC and sequence similarity with IKK1. Growth, morphogenesis, multiplication,  
 CC enlargement, differentiation and maturation of plant cells can be  
 CC modified by transforming them with nucleic acid encoding CDK inhibitor or  
 CC antisense construct complementary to the inhibitor gene, operably linked  
 CC to a tissue-specific promoter. The transgenic plants exhibit alteration  
 CC of traits such as petals, male sterility and ability to set seeds  
 XX  
 SQ Sequence 824 BP; 287 A; 164 C; 185 G; 188 T; 0 U; 0 Other;

Query Match 97.9%; Score 612.8; DB 3; Length 824;  
 Best Local Similarity 99.7%; Pred. No. 3.8e-179;  
 Matches 614; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 11 ACCCAAAAATCCAGAGAGAAAAAATGAGCGAGAGAAAGCGAGAGCTTGCGAAGAGC 70  
 DB 24 ACACAAAATCCAGAGAGAAAAAATGAGCGAGAGAAAGCGAGAGCTTGCGAAGAGC 83  
 QY 71 TTCAAGCACAAGCTTCTCACCACCTGAAGAAAACGAAGCTTAATGATCTTCTGATTTCATC 130  
 DB 84 TTCAAGCACAAGCTTCTCACCACCTGAAGAAAACGAAGCTTAATGATCTTCTGATTTCATC 143  
 QY 131 ACCGACTCTCATGACGTCATCGTCTTCGCGGTTTCATCTTCTTCGTTGTTTCGTCGCGC 190  
 DB 144 ACCGACTCTCATGACGTCATCGTCTTCGCGGTTTCATCTTCTTCGTTGTTTCGTCGCGC 203  
 QY 191 GGCTTTAGCGTCTCATGATGATTCGCTTACCATCGGTGGAGAAAGTGTATCAGTCCTC 250  
 DB 204 GGCTTTAGCGTCTCATGATGATGATTCGCTTACCATCGGTGGAGAAAGTGTATCAGTCCTC 263  
 QY 251 GAGTATCAGTCCCGTTGTTTTCACAGTGAATCGAAAGAAATCGCGAAGAACAGTTCGTC 310  
 DB 264 GAGTATCAGTCCCGTTGTTTTCACAGTGAATCGAAAGAAATCGCGAAGAACAGTTCGTC 323  
 QY 311 GTTTGGTGTAGATCTGGAGGATCATCAATCGAAACCGAAACCGAAACCTCAACATTCAT 370

Db 324 GTTTGGTGTAGTCTCGAGGATCATCAATCGAAACCGAAACCGAAACCTCAACATTCAT 383  
 QY 371 CACCAGCAATTTTCAGAAAAAGACGAGTCCAGTGAAGTGGGGTGGGAGAAACGACAAAC 430  
 Db 384 CACCAGCAATTTTCAGAAAAAGACGAGTCCAGTGAAGTGGGGTGGGAGAAACGACAAAC 443  
 QY 431 AGAATGGAATCATCTATCGGCAACGAAAGAAACAAACCGGGGGTGGGAGAACTTCAAC 490  
 Db 444 AGAATGGAATCATCTATCGGCAACGAAAGAAACAAACCGGGGGTGGGAGAACTTCAAC 503  
 QY 491 GCGCGGGAGATTGAGGATTTGTTCTCGGAGCTAGAGATCCAGACGATAAGAAAGCA 550  
 Db 504 GCGCGGGAGATTGAGGATTTGTTCTCGGAGCTAGAGATCCAGACGATAAGAAAGCA 563  
 QY 551 ATTCTAGAAAAAGTCAACTTCGATATTGTCAATGACGAAACCGCTTTGAAGGTCGCTACAA 610  
 Db 564 ATTCTAGAAAAAGTCAACTTCGATATTGTCAATGACGAAACCGCTTTGAAGGTCGCTACAA 623  
 QY 611 GTGGGATCGACTTTAA 626  
 Db 624 GTGGGATCGACTTTAA 639

RESULT 3

AAD40765  
 ID AAD40765 standard; cDNA; 824 BP.  
 XX  
 AC AAD40765;  
 XX  
 DT 30-OCT-2002 (first entry)  
 XX  
 DE Arabidopsis thaliana ICN2 cDNA.  
 XX  
 KW Plant development; cyclin-dependent kinase; CDK inhibitor; ICN1; ICN2;  
 KW ICN6; ICN7; ICN8; ICN9; ICN10; morphogenesis; maturation; enlargement;  
 KW plant breeding; growth; gene; ss.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 FH Key Location/Qualifiers  
 CDS 1..639  
 FT /\*tag= a  
 FT /product= "ICN2 protein #1"  
 FT /note= "No start codon"  
 FT /partial  
 CDS 49..639  
 FT /\*tag= b  
 FT /product= "ICN2 protein #2"  
 XX  
 PN WO200250292-A2.  
 XX  
 PD 27-JUN-2002.  
 XX  
 PF 18-DEC-2001; 2001WO-CA001825.  
 XX  
 PR 18-DEC-2000; 2000US-0255908P.  
 XX  
 PA (MIAC ) CANADA MIN AGRIC & AGRI-FOOD CANADA.  
 PA (UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.  
 XX  
 PI Wang H, Zhou Y, Fowke LC;  
 XX  
 DR WPI; 2002-519888/55.  
 DR P-PSDB; AAE25103, AAE25104.  
 XX  
 PT Modifying plant development, e.g. growth or maturation, which is  
 PT particularly useful in plant breeding, by introducing nucleic acids  
 PT coding for cyclin-dependent kinase (CDK) inhibitor, cyclin or proteins  
 PT that bind to CDK inhibitors.  
 XX  
 PS Disclosure; Fig 4; 89pp; English.  
 XX

CC The invention relates to a method for the development of a plant. The  
 CC method involves introducing into a plant cell a nucleic acid encoding a  
 CC protein that binds or interacts with a cyclin-dependent kinase (CDK)  
 CC inhibitor polypeptide (such as ICN1, ICN2, ICN6, ICN7, ICN8 and  
 CC ICN9), a cyclin polypeptide, a CDK, or a polypeptide that modulates the  
 CC degradation of a CDK inhibitor polypeptide. The method is useful for  
 CC modifying the growth and development of plants e.g. morphogenesis,  
 CC growth, multiplication, enlargement, differentiation or maturation of a  
 CC cell or plant. It is particularly useful in plant breeding. The present  
 CC sequence is A. thaliana ICN2 cDNA  
 XX  
 SQ Sequence 824 BP; 287 A; 164 C; 185 G; 188 T; 0 U; 0 Other;  
 Query Match 97.9%; Score 612.8; DB 6; Length 824;  
 Best Local Similarity 99.7%; Pred. No. 3.8e-179;  
 Matches 614; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 11 ACCCAAAATCCAAAGAGAGAAAAAATGAGCGAGAGAAAGAGAGAGCTTTCGACGAAGC 70  
 Db 24 ACACAAAATCCAAAGAGAGAAAAAATGAGCGAGAGAAAGAGAGCTTTCGACGAAGC 83  
 QY 71 TTCAAGCAACAGCTTCTCACCACTGAAGAAAAAGAGCTTAAATGATTTCTTCTGATCATC 130  
 Db 84 TTCAAGCAACAGCTTCTCACCACTGAAGAAAAAGAGCTTAAATGATTTCTTCTGATCATC 143  
 QY 131 ACCGACTCTCATGACGTCATCGTCTTCGCGGTTTCATCTTCTTCGTTCTTCGTCGGC 190  
 Db 144 ACCGACTCTCATGACGTCATCGTCTTCGCGGTTTCATCTTCTTCGTTCTTCGTCGGC 203  
 QY 191 GCGTTTAGCGTCTGATGATGTTCCGTTTACCATCGTGAGAGAAAGATGATCAGTCCCTC 250  
 Db 204 GCGTTTAGCGTCTGATGATGTTCCGTTTACCATCGTGAGAGAAAGATGATCAGTCCCTC 263  
 QY 251 GAGTATCAGCTCCGGTTGTTTCCACAGTGAATCGAAAGAAATCGCGAAGAACAGTTTCGTC 310  
 Db 264 GAGTATCAGCTCCGGTTGTTTCCACAGTGAATCGAAAGAAATCGCGAAGAACAGTTTCGTC 323  
 QY 311 GTTTCGTTGATGATCTGGAGGATCATCAATCGAAACCGAAACCTCAACATTCAT 370  
 Db 324 GTTTCGTTGATGATCTGGAGGATCATCAATCGAAACCGAAACCTCAACATTCAT 383  
 QY 371 CACCAGCAATTTTCAGAAAAAGACGAGTCCAGTGAAGTGGGGTGGGAGAAACGACAAAC 430  
 Db 384 CACCAGCAATTTTCAGAAAAAGACGAGTCCAGTGAAGTGGGGTGGGAGAAACGACAAAC 443  
 QY 431 AGAATGGAATCATCTATCGGCAACGAAAGAAACAAACCGGGGGTGGGAGAACTTCAAC 490  
 Db 444 AGAATGGAATCATCTATCGGCAACGAAAGAAACAAACCGGGGGTGGGAGAACTTCAAC 503  
 QY 491 GCGCGGGAGATTGAGGATTTGTTCTCGGAGCTAGAGATCCAGACGATAAGAAAGCA 550  
 Db 504 GCGCGGGAGATTGAGGATTTGTTCTCGGAGCTAGAGATCCAGACGATAAGAAAGCA 563  
 QY 551 ATTCTAGAAAAAGTCAACTTCGATATTGTCAATGACGAAACCGCTTTGAAGGTCGCTACAA 610  
 Db 564 ATTCTAGAAAAAGTCAACTTCGATATTGTCAATGACGAAACCGCTTTGAAGGTCGCTACAA 623  
 QY 611 GTGGGATCGACTTTAA 626  
 Db 624 GTGGGATCGACTTTAA 639  
 RESULT 4  
 AAZ29418  
 ID AAZ29418 standard; cDNA; 642 BP.  
 XX  
 AC AAZ29418;  
 XX  
 DT 29-FEB-2000 (first entry)  
 XX  
 DE Arabidopsis thaliana CDK inhibitor, ICN6 encoding cDNA.  
 XX  
 KW Cyclin-Dependent kinase inhibitor; CDK; Interactor of Cyclin 6; ICN6;

461 AAAACAACCGGGGTGAGGAAGA-----CTCCAACGGCGGGAGAT 502

The invention relates to a method for the development of a plant. The method involves introducing into a plant cell a nucleic acid encoding a protein that binds or interacts with a cyclin-dependent kinase (CDK) inhibitor polypeptide (such as ICK1, ICK2, ICK6, ICK7, ICK8 and ICK9), a cyclin polypeptide, a CDK, or a polypeptide that modulates the degradation of a CDK inhibitor polypeptide. The method is useful for modifying the growth and development of plants e.g. morphogenesis, growth, multiplication, enlargement, differentiation or maturation of a cell or plant. It is particularly useful in plant breeding. The present

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XX PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX Klein TM, Weng Z, Cahoon RE;
XX PI
XX DR WPI; 2000-679375/66.
XX P-PSDB; AAB27257.
XX
XX Cyclin dependent kinase inhibitor sequences, useful for identifying
XX herbicides and plant growth inhibitors.
XX
XX Claim 2; Page 52; 58pp; English.
XX
XX The present sequence is the coding sequence for the soybean cyclin-
XX dependent kinase inhibitor (CDKI). It was isolated by searching a soybean-
XX cDNA library for sequences similar to those encoding the CDKI from
XX Chenopodium rubrum, Caenorhabditis elegans and Arabidopsis thaliana. CDKI
XX is involved in the cell cycle, and may promote or inhibit cell division
XX and growth. The coding sequence and the protein it encodes are useful in
XX the production of transgenic plants which produce increased or decreased
XX amounts of the CDKI protein, in the identification of herbicides, in
XX genetic and physical mapping and in the isolation of the CDKI gene in
XX other organisms
XX
XX Sequence 467 BP; 158 A; 93 C; 95 G; 121 T; 0 U; 0 Other;
XX
XX Query Match 8.3%; Score 52; DB 3; Length 467;
XX Best Local Similarity 65.1%; Pred No. 2.3e-05;
XX Matches 95; Conservative 0; Mismatches 45; Indels 6; Gaps 1
XX
XX QY 477 AGGAAGACTCCAACGCGCGGAGATTGAGGATTTGTTTCTCGAGCTAGAGAGTCCAGAC 536
XX DB 146 AGAATATTTCCAAACGGCTTATGAGATGGAGGATTTCTTGTCTATGCTGAGA-----AG 199
XX
XX QY 537 GATAGAGAAGCAATTCATGAAAGTACAACTTCGATATTGTCATGACGACGCCGCTT 596
XX DB 200 CAGCAACAGACAATATTTATGACAAGTACAAATTCGACATTGTCAATGACGTACCTCTG 259
XX
XX QY 597 GAAGGTCGCTACAAGTGGGATCGACT 622
XX DB 260 CCTGGACGTACGAGTGGGTCCAGT 285
XX
XX RESULT 7
XX AAN02392
XX ID AAN02392 standard; DNA; 424 BP.
XX
XX AAN02392;
XX
XX 01-NOV-2001 (first entry)
XX
XX Soybean Cyclin dependent kinase inhibitor (CDKI) clone sl2.pk0008.d2.
XX
XX Cyclin dependent kinase inhibitor; CDKI; herbicide; cell cycle; soybean;
XX plant growth inhibitor; ds.
XX
XX Glycine max.
XX
XX Key Location/Qualifiers
XX CDS 2..118
XX FT FT /*tag= a
XX FT FT /product= "CDKI fragment"
XX FT FT /partial
XX FT FT /note= "No start codon given"
XX
XX WO200060087-A2.
XX
XX 12-OCT-2000.
XX
XX 06-APR-2000; 2000WO-US009106.
XX
XX 07-APR-1999; 99US-0128192P.
XX

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PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX Klein TM, Weng Z, Cahoon RE;
XX
XX
DR WPI; 2000-679375/66.
DR P-PSDB; AAP01942.
XX
XX Cyclin dependent kinase inhibitor sequences, useful for identifying
XX herbicides and plant growth inhibitors.
XX
XX Claim 10; Page 42; 58pp; English.
XX
XX The invention describes a novel isolated polynucleotide comprising a
XX nucleotide sequence encoding one of 17 specific cyclin dependent kinase
XX inhibitor (CDKI) polypeptides, cell cycle regulators involved in control
XX of cell division, growth and death. The nucleotide sequences can be used
XX in a vector to transform a host cell to produce the CDKI polypeptide.
XX They can also be used in methods for selecting and obtaining a nucleic
XX acid sequence that encodes CDKI or affects the level of CDKI expression.
XX The encoded protein can be used in a method for evaluating a compound for
XX its ability to inhibit the activity of a CDKI. The inhibitors can be used
XX as herbicides. They can also be used to inhibit plant growth. The
XX polynucleotide sequences can be used in gene mapping and as genetic
XX markers. The sequence encodes the soybean CDKI clone s12.pk0008.d2 as
XX described in the method of the invention
XX
SQ Sequence 424 BP; 120 A; 73 C; 83 G; 132 T; 0 U; 16 Other;
Query Match 7.8%; Score 48.8; DB 3; Length 424;
Best Local Similarity 73.8%; Pred. No. 0.00022;
Matches 62; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 535 ACGATAAGAGGAAGCAATTTCATAGAAAAGTACAACCTTCGATATTGTCAATGACGAAACCGC 594
DB 21 AGGACATTCAGAACGATTTCAAGACAAGTACAATTATGATATTGTTAAGACGTACCAC 80
QY 595 TTGAAGTCGCTACAAGTGGGATC 618
DB 81 TGGGAAGGACGCTACGAGTGGGTTTC 104
RESULT 8
AAA95278
ID AAA95278 standard; cDNA; 424 BP.
AC AAA95278;
XX
XX 17-JAN-2001 (first entry)
XX Soybean cyclin-dependent kinase inhibitor coding sequence #1.
XX
XX Soybean; cyclin-dependent kinase inhibitor; cell cycle; cell division;
XX CDKI; cell growth; herbicide; ss.
XX Glycine max.
XX Key Location/Qualifiers
XX CDS 2..118
XX /*tag= a
XX /product= "CDKI"
XX /partial
XX
XX WO200060087-A2.
XX
XX 12-OCT-2000.
XX
XX 06-APR-2000; 2000WO-US009106.
XX
XX 07-APR-1999; 99US-0128192P.
XX
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX Klein TM, Weng Z, Cahoon RE;
XX
XX WPI; 2000-679375/66.
XX Cyclin dependent kinase inhibitor sequences, useful for identifying
XX herbicides and plant growth inhibitors.
XX
XX Claim 2; Page 41-42; 58pp; English.
XX
XX The present sequence is the coding sequence for the soybean cyclin-
XX dependent kinase inhibitor (CDKI). It was isolated by searching a soybean
XX seedling cDNA library for sequences similar to those encoding the CDKI
XX from Chenopodium rubrum, Caenorhabditis elegans and Arabidopsis thaliana.
XX CDKI is involved in the cell cycle, and may promote or inhibit cell
XX division and growth. The coding sequence and the protein it encodes are
XX useful in the production of transgenic plants which produce increased or
XX decreased amounts of the CDKI protein, in the identification of
XX herbicides, in genetic and physical mapping and in the isolation of the
XX CDKI gene in other organisms
XX
SQ Sequence 424 BP; 120 A; 73 C; 83 G; 132 T; 0 U; 16 Other;
Query Match 7.8%; Score 48.8; DB 3; Length 424;
Best Local Similarity 73.8%; Pred. No. 0.00022;
Matches 62; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 535 ACGATAAGAGGAAGCAATTTCATAGAAAAGTACAACCTTCGATATTGTCAATGACGAAACCGC 594
DB 21 AGGACATTCAGAACGATTTCAAGACAAGTACAATTATGATATTGTTAAGACGTACCAC 80
QY 595 TTGAAGTCGCTACAAGTGGGATC 618
DB 81 TGGGAAGGACGCTACGAGTGGGTTTC 104
RESULT 9
AAA95287
ID AAA95287 standard; cDNA; 620 BP.
AC AAA95287;
XX
XX 17-JAN-2001 (first entry)
XX Soybean cyclin-dependent kinase inhibitor coding sequence #2.
XX
XX Soybean; cyclin-dependent kinase inhibitor; cell cycle; cell division;
XX CDKI; cell growth; herbicide; ss.
XX Glycine max.
XX Key Location/Qualifiers
XX CDS 1..264
XX /*tag= a
XX /product= "CDKI"
XX /partial
XX
XX WO200060087-A2.
XX
XX 12-OCT-2000.
XX
XX 06-APR-2000; 2000WO-US009106.
XX
XX 07-APR-1999; 99US-0128192P.
XX
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX Klein TM, Weng Z, Cahoon RE;
XX
XX WPI; 2000-679375/66.
XX Cyclin dependent kinase inhibitor sequences, useful for identifying
XX herbicides and plant growth inhibitors.
XX
XX

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PS Claim 2; Page 49; 58pp; English.

CC The present sequence is the coding sequence for the soybean cyclin-  
 CC dependent kinase inhibitor (CDKI). It was isolated by searching a soybean  
 CC seedling cDNA library for sequences similar to those encoding the CDKI  
 CC from *Chenopodium rubrum*, *Caenorhabditis elegans* and *Arabidopsis thaliana*.  
 CC CDKI is involved in the cell cycle, and may promote or inhibit cell  
 CC division and growth. The coding sequence and the protein it encodes are  
 CC useful in the production of transgenic plants which produce increased or  
 CC decreased amounts of the CDKI protein, in the identification of  
 CC herbicides, in genetic and physical mapping and in the isolation of the  
 CC CDKI gene in other organisms

SQ Sequence 620 BP; 191 A; 111 C; 134 G; 183 T; 0 U; 1 Other;

Query Match 7.8%; Score 48.8; DB 3; Length 620;  
 Best Local Similarity 73.8%; Pred. No. 0.00026;  
 Matches 62; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 535 ACGATAAGAGAGCAATTCATAGAAAGTACAACTTCGATATTTGTCATGTAGCAACCGC 594  
 DB 167 AGGACATTCAGAAACGATTTCAAGACAGTACAAATATGATATTTGTTAAGGACGTACCAC 226

QY 595 TTGAAGTGCCTACAGTGGGATC 618  
 DB 227 TGGAGGRCGCTACGAGTGGGTTTC 250

RESULT 10

AA02401  
 ID AA02401 standard; DNA; 620 BP.

XX AC AA02401;

XX 01-NOV-2001 (first entry)

DE Cyclin dependent kinase inhibitor (CDKI) clone sl2.pk0008.d2.fis.

XX Cyclin dependent kinase inhibitor; CDKI; herbicide; cell cycle; soybean;

KW plant growth inhibitor; ds.

XX Glycine max.

OS

FH Key Location/Qualifiers

FT CDS 1..264

FT /\*tag= a

FT /product= "CDKI fragment"

FT /partial

FT /note= "No start codon given"

XX WO200060087-A2.

PN 12-OCT-2000.

XX 06-APR-2000; 2000WO-US009106.

XX 07-APR-1999; 99US-0128192P.

XX (DUPO ) DU PONT DE NEMOURS & CO E I.

XX Klein TM, Weng Z, Cahoon RE;

XX WPI; 2000-679375/66.

DR P-PSDB; AAP01951.

XX Cyclin dependent kinase inhibitor sequences, useful for identifying  
 PT herbicides and plant growth inhibitors.

XX Claim 2; Page 49; 58pp; English.

CC The invention describes a novel isolated polynucleotide comprising a  
 CC nucleotide sequence encoding one of 17 specific cyclin dependent kinase  
 CC inhibitor (CDKI) polypeptides, cell cycle regulators involved in control  
 CC of cell division, growth and death. The nucleotide sequences can be used  
 CC in a vector to transform a host cell to produce the CDKI polypeptide.  
 CC They can also be used in methods for selecting and obtaining a nucleic  
 CC acid sequence that encodes CDKI or affects the level of CDKI expression.

CC of cell division, growth and death. The nucleotide sequences can be used  
 CC in a vector to transform a host cell to produce the CDKI polypeptide.  
 CC They can also be used in methods for selecting and obtaining a nucleic  
 CC acid sequence that encodes CDKI or affects the level of CDKI expression.  
 CC The encoded protein can be used in a method for evaluating a compound for  
 CC its ability to inhibit the activity of a CDKI. The inhibitors can be used  
 CC as herbicides. They can also be used to inhibit plant growth. The  
 CC polynucleotide sequences can be used in gene mapping and as genetic  
 CC markers. The sequence encodes the soybean CDKI clone sl2.pk0008.d2.fis as  
 CC described in the method of the invention

SQ Sequence 620 BP; 191 A; 111 C; 134 G; 183 T; 0 U; 1 Other;

Query Match 7.8%; Score 48.8; DB 3; Length 620;  
 Best Local Similarity 73.8%; Pred. No. 0.00026;  
 Matches 62; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 535 ACGATAAGAGAGCAATTCATAGAAAGTACAACTTCGATATTTGTCATGTAGCAACCGC 594  
 DB 167 AGGACATTCAGAAACGATTTCAAGACAGTACAAATATGATATTTGTTAAGGACGTACCAC 226

QY 595 TTGAAGTGCCTACAGTGGGATC 618  
 DB 227 TGGAGGRCGCTACGAGTGGGTTTC 250

RESULT 11

AA02402  
 ID AA02402 standard; DNA; 1116 BP.

XX AC AA02402;

XX 01-NOV-2001 (first entry)

DE Cyclin dependent kinase inhibitor (CDKI) clone sdp4c.pk025.k23.

XX Cyclin dependent kinase inhibitor; CDKI; herbicide; cell cycle; soybean;

KW plant growth inhibitor; ds.

XX Glycine max.

OS

FH Key Location/Qualifiers

FT CDS 143..760

FT /\*tag= a

FT /product= "CDKI"

XX WO200060087-A2.

PN 12-OCT-2000.

XX 06-APR-2000; 2000WO-US009106.

XX 07-APR-1999; 99US-0128192P.

XX (DUPO ) DU PONT DE NEMOURS & CO E I.

XX Klein TM, Weng Z, Cahoon RE;

XX WPI; 2000-679375/66.

DR P-PSDB; AAP01952.

XX Cyclin dependent kinase inhibitor sequences, useful for identifying  
 PT herbicides and plant growth inhibitors.

XX Claim 2; Page 49-50; 58pp; English.

CC The invention describes a novel isolated polynucleotide comprising a  
 CC nucleotide sequence encoding one of 17 specific cyclin dependent kinase  
 CC inhibitor (CDKI) polypeptides, cell cycle regulators involved in control  
 CC of cell division, growth and death. The nucleotide sequences can be used  
 CC in a vector to transform a host cell to produce the CDKI polypeptide.  
 CC They can also be used in methods for selecting and obtaining a nucleic  
 CC acid sequence that encodes CDKI or affects the level of CDKI expression.

CC The encoded protein can be used in a method for evaluating a compound for  
 CC its ability to inhibit the activity of a CDKI. The inhibitors can be used  
 CC as herbicides. They can also be used to inhibit plant growth. The  
 CC polynucleotide sequences can be used in gene mapping and as genetic  
 CC markers. The sequence encodes the soybean CDKI clone sdp4c.pk025.k23 as  
 CC described in the method of the invention

SQ Sequence 1116 BP; 339 A; 236 C; 269 G; 272 T; 0 U; 0 Other;  
 Query Match 7.5%; Score 47.2; DB 3; Length 1116;  
 Best Local Similarity 72.6%; Pred. No. 0.0011;  
 Matches 61; Conservative 0; Mismatches 23; Indels 0; Gaps 0;  
 QY 535 ACGATAAGAGAACGAATTCATAGAAAAGTACAACTTCGATATTGTCATATGACGACCGC 594  
 DB 663 AAGACATTCAGAAACGATTTCAAGACAGATACATATGATATTGTTAAGGACGTACCGC 722  
 QY 595 TTGAAGTCGCTACAAAGTGGGATC 618  
 DB 723 TGGAAGGACGCTACGAGTGGGTTT 746

RESULT 12  
 AAA95288  
 ID AAA95288 standard; cDNA; 1116 BP.  
 AC AAA95288;  
 DT 17-JAN-2001 (first entry)  
 DE Soybean cyclin-dependent kinase inhibitor coding sequence #3.  
 KW Soybean; cyclin-dependent kinase inhibitor; cell cycle; cell division;  
 KW CDKI; cell growth; herbicide; ss.  
 OS Glycine max.

Key Location/Qualifiers  
 CDS 143..760  
 FT /\*tag= a  
 FT /product= "CDKI"  
 WO2000060087-A2.  
 12-OCT-2000.  
 06-APR-2000; 2000WO-US009106.  
 07-APR-1999; 99US-0128192P.  
 (DUPO ) DU PONT DE NEMOURS & CO E I.  
 Klein TM, Weng Z, Cahoon RE;  
 WPI; 2000-679375/66.  
 P-PSDB; AAB27254.

Cyclin dependent kinase inhibitor sequences, useful for identifying  
 herbicides and plant growth inhibitors.  
 Claim 2; Page 49-50; 58pp; English.

The present sequence is the coding sequence for the soybean cyclin-  
 dependent kinase inhibitor (CDKI). It was isolated by searching a soybean  
 pod cDNA library for sequences similar to those encoding the CDKI from  
 Chenopodium rubrum, Caenorhabditis elegans and Arabidopsis thaliana. CDKI  
 is involved in the cell cycle, and may promote or inhibit cell division  
 and growth. The coding sequence and the protein it encodes are useful in  
 the production of transgenic plants which produce increased or decreased  
 amounts of the CDKI protein, in the identification of herbicides, in  
 genetic and physical mapping and in the isolation of the CDKI gene in  
 other organisms

SQ Sequence 1116 BP; 339 A; 236 C; 269 G; 272 T; 0 U; 0 Other;  
 Query Match 7.5%; Score 47.2; DB 3; Length 1116;  
 Best Local Similarity 72.6%; Pred. No. 0.0011;  
 Matches 61; Conservative 0; Mismatches 23; Indels 0; Gaps 0;  
 QY 535 ACGATAAGAGAACGAATTCATAGAAAAGTACAACTTCGATATTGTCATATGACGACCGC 594  
 DB 663 AAGACATTCAGAAACGATTTCAAGACAGATACATATGATATTGTTAAGGACGTACCGC 722  
 QY 595 TTGAAGTCGCTACAAAGTGGGATC 618  
 DB 723 TGGAAGGACGCTACGAGTGGGTTT 746

RESULT 13  
 AA229420  
 ID AA229420 standard; cDNA; 804 BP.  
 AC AA229420;  
 DT 29-FEB-2000 (first entry)  
 DE Chenopodium rubrum CDKI1 encoding cDNA.  
 KW Cyclin-Dependent kinase; CDK; CDKI1; Cdc2a; D-class cyclin; CycD1; CycD2;  
 KW CycD3; morphogenesis; transgenic plant; male sterility; ds.  
 OS Chenopodium rubrum.

Key Location/Qualifiers  
 CDS 58..648  
 FT /\*tag= a  
 FT /product= "CDKI1"  
 WO9964599-A1.  
 16-DEC-1999.  
 08-JUN-1999; 99WO-CA000532.  
 08-JUN-1998; 98CA-02235978.  
 31-DEC-1998; 98CA-02256121.  
 (MIAC ) AGRIC & AGRIFOOD CANADA.  
 (UYSA ) UNIV SASKATCHEWAN TECHNOLOGIES INC.  
 (CANA ) NAT RES COUNCIL CANADA.

Wang H, Fowke LC, Crosby WL;  
 WPI; 2000-097540/08.  
 P-PSDB; AAY44340.  
 Modifying plant cell development using nucleic acid encoding inhibitor of  
 cyclin-dependent kinase, or corresponding antisense sequence, e.g. for  
 inducing male sterility.  
 Disclosure; Fig 6; 58pp; English.

The present sequence is a cDNA encoding C. rubrum CDKI1, which inhibits  
 Arabidopsis thaliana Cyclin-Dependent kinase (CDK). CDKI1 interacts with  
 Cdc2a, D-class cyclins, CycD1, CycD2 and CycD3 and shares functional and  
 sequence similarity with ICK1. Growth, morphogenesis, multiplication,  
 enlargement, differentiation and maturation of plant cells can be  
 modified by transforming them with Agrobacterium strain harbouring an  
 expression construct of CDKI1. The transgenic plants exhibit alteration  
 of traits such as petals, male sterility and ability to set seeds

SQ Sequence 804 BP; 254 A; 151 C; 202 G; 197 T; 0 U; 0 Other;  
 Query Match 7.4%; Score 46.2; DB 3; Length 804;  
 Best Local Similarity 59.2%; Pred. No. 0.0019;  
 Matches 100; Conservative 0; Mismatches 63; Indels 6; Gaps 1;



Qy	533	AGACGATAAGAAAGCAATTTCATAGAAAAAGTACAACTTCGATATTGTCAATGACGAACC	592
Db	241	ACTC-----AAAGAAAAATTCAGAAGAAGTACAAATTCGATTTTCGAGAGGAGAAGCC	294
Qy	593	GCTTGAAGTCCGTACAAGTGGG	615
Db	295	ATTAGAGGACGTTACGAATGGG	317

Search completed: September 30, 2005, 09:13:53  
Job time : 478 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 30, 2005, 09:05:51 ; Search time 163 Seconds  
(without alignments)  
6284.106 Million cell updates/sec

Title: US-09-980-758A-7  
Perfect score: 626  
Sequence: 1 ctcgagattaccacaaaat.....acaagtgggacgacttta 626

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.\*  
1: /cgn2\_6/ptodata/1/ina/5A COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5B COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	58	9.3	7218	1	Sequence 14, Appl
C 2	43	6.9	875	4	Sequence 2, Appl
C 3	41.8	6.7	505	4	Sequence 15639, A
C 4	40.8	6.5	1193	4	Sequence 5, Appl
C 5	38.2	6.1	3143	1	Sequence 1, Appl
C 6	38.2	6.1	3143	2	Sequence 1, Appl
C 7	38.2	6.1	3143	5	Sequence 1, Appl
C 8	36.6	5.8	1371	4	Sequence 5113, Ap
C 9	35.6	5.7	738	4	Sequence 1525, Ap
C 10	35.6	5.7	7760	3	Sequence 68, App
C 11	35.2	5.6	265	4	Sequence 13444, A
C 12	35	5.6	467	4	Sequence 3165, Ap
C 13	35	5.6	467	4	Sequence 7933, Ap
C 14	35	5.6	954	4	Sequence 23215, A
C 15	35	5.6	1104	4	Sequence 608, App
C 16	34.6	5.5	172677	4	Sequence 13444, A
C 17	34.6	5.5	998	3	Sequence 5, Appl
C 18	34	5.4	1817	4	Sequence 4363, Ap
C 19	33.8	5.4	29172	4	Sequence 15520, A
C 20	33.6	5.4	1866	4	Sequence 66, Appl
C 21	33.4	5.3	522	4	Sequence 1015, Ap
C 22	33.4	5.3	522	4	Sequence 2269, Ap
C 23	33.4	5.3	540	3	Sequence 1400, Ap
C 24	33.4	5.3	2945	4	Sequence 4019, Ap
C 25	33.4	5.3	3123	4	Sequence 3699, Ap
C 26	33.4	5.3	3697	4	Sequence 4317, Ap
C 27	33.4	5.3	3726	4	Sequence 3917, Ap

Query Match 9.3%; Score 58; DB 1; Length 7218;

Sequence 17, Appl  
Sequence 17, Appl  
Sequence 14497, A  
Sequence 2807, Ap  
Sequence 2739, Ap  
Sequence 18033, A  
Sequence 184864,  
Sequence 184865,  
Sequence 184866,  
Sequence 184867,  
Sequence 184868,  
Sequence 184869,  
Sequence 184870,  
Sequence 184871,  
Sequence 185019,  
Sequence 185020,  
Sequence 185021,  
Sequence 185022,

## ALIGNMENTS

RESULT 1  
US-08-232-463-14/c  
; Sequence 14, Application US/08232463  
; Patent No. 5670367  
; GENERAL INFORMATION:  
; APPLICANT: DORNER, F.  
; APPLICANT: SCHEIFLINGER, F.  
; APPLICANT: FALKNER, F. G.  
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 1800 Diagonal Road, Suite 500  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22313-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/232.463  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/935.313  
; FILING DATE:  
; APPLICATION NUMBER: EP 91 114 300.6  
; FILING DATE: 26-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)836-9300  
; TELEFAX: (703)683-4109  
; TELEX: 899149  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7218 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; CLONE: ptzgpt-F1s  
US-08-232-463-14

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Best Local Similarity 1.2%; Pred. No. 1.2e-07;
Matches 4; Conservative 215; Mismatches 125; Indels 0; Gaps 0;
QY 276 AGTGAATCGAAGAAATCGGAAGAACAGTTCGTGTTGGTGTAGATCTGGAGGATCAT 335
Db 1406 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1347
QY 336 CAAATCGAAACCGAACCGAACCTCAACATTCACAGCAATTCAGAAAAGAGACG 395
Db 1346 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1287
QY 396 AGTCAGTCAGTGAGGTTTGGGAGAACGACAGAAATGGAATCATCTCGGCAACG 455
Db 1286 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1227
QY 456 AAGAGAAACAAACCGGGGTGAGGAAGACTCCAAACGCGCGGAGATTGAGGATTTGTC 515
Db 1226 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1167
QY 516 TCGGAGCTAGAGAGTCCAGACGATAAGAGCAATTCATAGAAAAGTACAACTTCGAT 575
Db 1166 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1107
QY 576 ATTGTCATGAGCAACCCCTTGAAGTCGCTACAAAGTCGGATCG 619
Db 1106 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRATCG 1063
```

## RESULT 2

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US-09-526-597D-3
; Sequence 3, Application US/09526597D
; Patent No. 6710227
; GENERAL INFORMATION:
; APPLICANT: De Veylder, Lieven
; APPLICANT: De Almeida, Janice
; APPLICANT: Landrieu, Isabelle
; TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof
; FILE REFERENCE: 1187-2
; CURRENT APPLICATION NUMBER: US/09/526,597D
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 3
; LENGTH: 875
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (11)..(658)
US-09-526-597D-3
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Query Match 6.9%; Score 43; DB 4; Length 875;
Best Local Similarity 69.9%; Pred. No. 0.0025;
Matches 58; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
QY 544 AGAAGCAATTCATAGAAAAGTACAACTTCGATATTGTCAATGACGAAACCGCTTGAAGTC 603
Db 573 AGAGCTATTTCATGAGAGTACAACTTCGATATTGTCAATGATATCCCTCAGCGGAC 632
QY 604 GCTACAAGTGGATCGAGCTTTAA 626
Db 633 GTTACGAATGGTGAAGTCAAA 655
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## RESULT 3

```
US-09-621-976-15639/c
; Sequence 15639, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
```

```
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 15639
; LENGTH: 505
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-15639
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Query Match 6.7%; Score 41.8; DB 4; Length 505;
Best Local Similarity 11.5%; Pred. No. 0.0043;
Matches 36; Conservative 153; Mismatches 120; Indels 4; Gaps 1;
QY 296 GAAGAACAGTTCGTCGTTGGTGTAGATCTCGAGGATCATCAATCGAAACCGAACCGA 355
Db 338 SMTKRRMMTYSGMMWTSYKCTKTKKYTGWKSKKTRWTCTSWRKYMMWMMGCVARSMSKS 279
QY 356 AACCTCAACATTCATCACAGCAATTTTCAGAAAAGAGACGAGTCCAGTGAGTGAGGGTTT 415
Db 278 WARSWYMMACWCMWSASAYRARRSMYCARSMRAGAGWRRARRGKRRKSSMMRSK 219
QY 416 GGGAGAAACGACAAACAGAAATGGAATCATCTCGGCAACGAGAGAAACAAACCGGGGT 475
Db 218 MSSRMSGAGKARCMCRMMWSCRRMSYCMGSKMSCRGTCAKMWRARYAKRYASSMGKY 159
QY 476 GAGGAAGACTCCAACG---CGCGCGGAGATTGAGGATTTGTTCTCGAGGCTAGAGATC 531
Db 158 MNGCRWCYAKCARMYGYYRSRSTGRGMKYYRRKMYMMKYMMWMMCYRMGAAMYGM 99
QY 532 CAGACGATAAGAGAAGCAATTCATAGAAAAGTACAACTTCGATATTGTCAATGACGAAC 591
Db 98 SARAYRMYASMSACKMCSRMMKMSWMMRCWRSRYRCWMSGKWCYSCCGYCCSACRMC 39
QY 592 CGCTTGAAGGTGCG 604
Db 38 YCWTRRMKMSWYSS 26
```

## RESULT 4

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US-09-526-597D-5
; Sequence 5, Application US/09526597D
; Patent No. 6710227
; GENERAL INFORMATION:
; APPLICANT: De Veylder, Lieven
; APPLICANT: De Almeida, Janice
; APPLICANT: Landrieu, Isabelle
; TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof
; FILE REFERENCE: 1187-2
; CURRENT APPLICATION NUMBER: US/09/526,597D
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 5
; LENGTH: 1193
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (92)..(763)
US-09-526-597D-5
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Query Match 6.5%; Score 40.8; DB 4; Length 1193;
Best Local Similarity 65.2%; Pred. No. 0.015;
Matches 60; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 533 AGACGATAAGAGAAGCAATTCATAGAAAAGTACAACTTCGATATTGTCAATGACGAAC 592
Db 664 AGCGAGCAGCAAGGAGTTCATGAGAGAGTACAACTTGTATCTGTGACAGACGCC 723
QY 593 GCTTGAAGGTGCGTTACAAAGTGGGATCGACTTT 624
```



; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gerhold, David L.
; APPLICANT: Strauss, Allison Cole
; TITLE OF INVENTION: Anti-fungal Agents and Methods of
; TITLE OF INVENTION: Identifying and Using the Same
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09530A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,621
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,399
; FILING DATE: 21-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1970
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3143 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: genomic DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 547..2889
PCT-US96-09530A-1

Query Match 6.1%; Score 38.2; DB 5; Length 3143;
Best Local Similarity 48.8%; Pred. No. 0.18;
Matches 103; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

Qy 328 AGGATCATCAATCGAAGCCGAAACCGAAACCTCAGATTTCATCCAGCAATTTTCAGAA 387
Db 788 AGGAACCTTAAAGTGCCCAATAAATCCAAATCTACATCTAAAAAGGACACCAAAAGTTAGA 847

Qy 388 AAGAGACGAGTCCAGTGTAGGGGTTTGGGAGAAACGACACAGAAATGGATCATCAT 447
Db 848 AAGAGAAACTACAGTCAAGAGGAATCTAAAGCCACAGCAGCTAAAGTGAAGAAGAAAT 907

Qy 448 CGGCAACGAGAGAAAAACAACGGGGGTGAGGAGAGACTCCAAACGGCGCGGAGATTGAGG 507
Db 908 CCAAAACTCAATCAGATTCAAGCATCGGTTAAATCTGAAACTCTCTGAAGAAGATCAAG 967

Qy 508 ATTTGTTCTCGAGCTAGAGAGTCCAGACGA 538
Db 968 GGTACAAATGTTGGGAAGTGAATCAAGAAGA 998

RESULT 8
US-09-248-796A-5113
; Sequence 5113, Application US/09248796A

; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 5113
; LENGTH: 1371
; TYPE: DNA
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1165)
; OTHER INFORMATION: Identity of nucleotide sequences at the above locations are unknc
US-09-248-796A-5113

Query Match 5.8%; Score 36.6; DB 4; Length 1371;
Best Local Similarity 48.3%; Pred. No. 0.37;
Matches 102; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

Qy 328 AGGATCATCAATCGAAGCCGAAACCGAAACCTCAACATTCATCACCAGCAATTTTCAGAA 387
Db 443 AGGAACCTTAAAGTGCCAGTAAATCCAAATCTACATCTAAAAAGGACACCAAAAGTTAGA 502

Qy 388 AAGAGACGAGTCCAGTGTAGGGGTTTGGGAGAAACGACAAATGGAATCATCAT 447
Db 503 AAGAGAAACTACAGTCAAGAGGAATCTAAAGCCACAAGCAGCTAAAGTGAAGAAGAAAT 562

Qy 448 CGGCAACGAGAGAAAAACAACGGGGGTGAGGAGAGACTCCAAACGGCGCGGAGATTGAGG 507
Db 563 CCAAAACTCAATCAGATTCAAGCATCGGTTAAATCTGAAACTCTTTGAAGAAGATCAAG 622

Qy 508 ATTTGTTCTCGAGCTAGAGAGTCCAGACGA 538
Db 623 GGTACAAATGTTGGGAAGTGAATCAAGAAGA 653

RESULT 9
US-09-583-110-1525/c
; Sequence 1525, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 1525
; LENGTH: 738
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-1525

Query Match 5.7%; Score 35.6; DB 4; Length 738;
Best Local Similarity 51.9%; Pred. No. 0.54;
Matches 80; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

Qy 282 TCGAAGAAATCGCGAAGACAGATTCGTCGTTGCTAGATCTGGAGGATCATCAAAATC 341



Db 276 TCATAAAACTGAGATGAACATTTTGGCTCTCTGTCAAAAATGAGTTTGTCAATCATTTTC 217  
QY 342 GAAACCGAAACCGAAACCTCAACATTCATCACCAGCAATTTTCAGAAAAAGAGACGAGTCCA 401  
Db 216 CACATAATCAGTACAACTGACTCATCACCACAGGAATGACTAAAGGGAGACCCGAC 157  
QY 402 GTGAGTGAGGGTTTGGGAAAGACGACAAAGAAA 435  
Db 156 TTGACGAATGATCTCTGCGAATCTACAAGATACA 123

RESULT 10  
US-08-961-527-63/c  
; Sequence 63, Application US/08961527  
; Patent No. 6420135  
; GENERAL INFORMATION:  
; APPLICANT: Charles Kunsch  
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences  
; NUMBER OF SEQUENCES: 391  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/961,527  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brookes, A. Anders  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PB340P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8512  
; INFORMATION FOR SEQ ID NO: 63:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7760 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
US-08-961-527-63

Query Match 5.7%; Score 35.6; DB 3; Length 7760;  
Best Local Similarity 51.9%; Pred. No. 2.1;  
Matches 80; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 282 TCGAAGAATCCGGAAGACAGTTCGTCTGTTGGTGTAGATCTGAGGATCATCAATTC 341  
Db 7588 TCATAAAACTGAGGATGAACATTTTGGCTCTCTGTCAAAAATGAGTTTGTCAATCATTTTC 7529

QY 342 GAAACCGAAACCGAAACCTCAACATTCATCACCAGCAATTTTCAGAAAAAGAGACGAGTCCA 401  
Db 7528 CACATAATCAGTACAACTGACTCATCACCACAGGAATGACTAAAGGGAGACCCGAC 7469

QY 402 GTGAGTGAGGGTTTGGGAAAGACGACAAAGAAA 435  
Db 7468 TTGACGAATGATCTCTGCGAATCTACAAGATACA 7435

; Sequence 3165, Application US/09313294A  
; Patent No. 6476212  
; GENERAL INFORMATION:  
; APPLICANT: Lalgudi, Raghunath V.  
; APPLICANT: Ito, Laura Y.  
; APPLICANT: Sherman, Bradley K.  
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR  
; FILE REFERENCE: PL-0017 US  
; CURRENT APPLICATION NUMBER: US/09/313,294A  
; CURRENT FILING DATE: 1999-05-14  
; NUMBER OF SEQ ID NOS: 7600  
; SOFTWARE: PERL Program  
; SEQ ID NO 3165  
; LENGTH: 265  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. 6476212 700611002H1  
US-09-313-294A-3165

Query Match 5.6%; Score 35.2; DB 4; Length 265;  
Best Local Similarity 68.1%; Pred. No. 0.4;  
Matches 49; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 544 AGAAGCAATTCATAGAAAAAGTACAACTTCGATATTGTCAATGACGACCGCTTGAAGTTC 603  
Db 16 AGCAGGATTCATTGACAAAGTACAACTTCGATTCCTGCAAAACGACTGCCCTCTCCAGGCA 75

QY 604 GCTACAAGTGGG 615  
Db 76 GGTTCGAGTGGG 87

RESULT 12  
US-09-270-767-7933  
; Sequence 7933, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7933  
; LENGTH: 467  
; TYPE: DNA  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-7933

Query Match 5.6%; Score 35; DB 4; Length 467;  
Best Local Similarity 50.3%; Pred. No. 0.64;  
Matches 86; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

QY 400 CAGTGAGTGAGGTTTGGGAGAAACGACAAACAGAAATGGAATCATCGGCAACGAAGA 459  
Db 187 CAAACAGTGTGTCGTGTGTAACCAAACTAAAAACCTACAAAGCAAGAAAAACGAAA 246

QY 460 GAAACACACCGGGGTGAGGAAGACTCCAAACGCGCGCGGAGATTGAGGATTTGTTCTCGG 519  
Db 247 AAAAAAACGAAACGAAACGAAAGGATAGTGCCTAAAAAGTGTATAATTCTGTATACCA 306

QY 520 AGCTAGAGAGTCCAGACCATAGAGAGCAATTCATAGAAAGTACAACT 570  
Db 307 AAGTCGAGAGATCTCTGTAAATTAGTCAAAAAAAGAAAAAAT 357

RESULT 13  
US-09-270-767-23215  
; Sequence 23215, Application US/09270767  
; Patent No. 6703491

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; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23215
; LENGTH: 467
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-23215

Query Match          5.6%; Score 35; DB 4; Length 467;
Best Local Similarity 50.3%; Pred. No. 0.64;
Matches 86; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

QY 400 CAGTGTGAGGGTTTGGAGAAACGACAAACGAAATCGAATCATCTCGGCAACGAGA 459
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 187 CAACAGTGTGTGCGTGTGTAACCAAACTTAAAAACCTACAGCAAGAAAAACGAAA 246

QY 460 GAAACACACGGGGTGTAGGAGACTCCACGGCGCGAGATTGAGGATTGTCTCGG 519
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 247 AAAAAAACGAAACGAAACGAAACGAGGATGTGCGCTAAAGTGATTAATCGTATACCA 306

QY 520 AGCTAGAGAGTCCAGACGATAGAAAGAGCAATTCTATAGAAAAAGTACAACT 570
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 307 AAGTCGAGAGTCTCTGTAATTAGTCAAAAAAGAAAAAGAAAAAT 357

RESULT 14
US-09-583-110-608/c
; Sequence 608, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 608
; LENGTH: 954
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-608

Query Match          5.6%; Score 35; DB 4; Length 954;
Best Local Similarity 52.4%; Pred. No. 0.98;
Matches 77; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 320 AGATCTGGAGGATCATCAATCGAAACCGAAACCTCAACATTCATCACCAGCAA 379
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Db 783 AGATCTCGGATTGCCCAAAATGAGGGTCCGAACCAACAAAAAAGGTTCATCAGCAGAGA 724

QY 380 TTTCAGAAAGACGACGAGTCCAGTGAGTGAGGTTTGGAGAAACGACAAACAGAAATGGA 439
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 723 AAGAAAAACAATAGGAGACCGAGCTACAAAGGCTATAGTCAAGGGAAATCTGAAAAATTT 664

QY 440 ATCATCATCGGCAACGAGAGAAAAACA 466
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Db 663 AACATCCCTTCAATGGAGTAAAAAAA 637
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RESULT 15

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US-09-107-433-686/c
; Sequence 686, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 686:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1104 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...1104
; SEQUENCE DESCRIPTION: SEQ ID NO: 686:
US-09-107-433-686

Query Match          5.6%; Score 35; DB 4; Length 1104;
Best Local Similarity 52.4%; Pred. No. 1.1;
Matches 77; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 320 AGATCTGAGGATCATCAAAATCGAAACCGAAACCGAAACCTCAACATTCATCACCAGCAA 379
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 933 AGATGTGCGATTGCCCAAAATGAGGGTCCGAACCAACAAAAAAGGTTCATCAGCAGAGA 874

QY 380 TTTCAGAAAGACGACGAGTCCAGTGAGTGAGGTTTGGAGAAAAACGACAAACAGAAATGGA 439
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 873 AAGAAAAACAATAGGAGACCGAGCTCAAAAGGCTATAGTCAAGGGAAATCTGAAAAATTT 814

QY 440 ATCATCATCGGCAACGAGAGAAAAACA 466
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 813 AACATCCCTTCAATGGAGTAAAAAAA 787

Search completed: September 30, 2005, 10:08:15
Job time : 164 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 30, 2005, 09:05:52 ; Search time 2173 Seconds  
(without alignments)  
1989.100 Million cell updates/sec

Title: US-09-980-758A-7  
Perfect score: 626  
Sequence: 1 CTCGGATTACCAAAAT.....ACAAGTGGATGACGCTTTAA 626

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 7442561 seqs, 3452328358 residues

Total number of hits satisfying chosen parameters: 14885122

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA.\*

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3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*  
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14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*  
15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*  
16: /cgn2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq.\*  
17: /cgn2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq.\*  
18: /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq.\*  
19: /cgn2\_6/ptodata/2/pubpna/US10G\_PUBCOMB.seq.\*  
20: /cgn2\_6/ptodata/2/pubpna/US10H\_PUBCOMB.seq.\*  
21: /cgn2\_6/ptodata/2/pubpna/US10I\_PUBCOMB.seq.\*  
22: /cgn2\_6/ptodata/2/pubpna/US10J\_NEW\_PUB.seq.\*  
23: /cgn2\_6/ptodata/2/pubpna/US11A\_PUBCOMB.seq.\*  
24: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
25: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*  
26: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					Description	
Result No.	Score	Query Match	Length	ID		
1	612.8	97.9	824	9	US-09-733-507-7	Sequence 7, Appli
2	612.8	97.9	824	18	US-10-451-139-7	Sequence 7, Appli
3	122	19.5	642	9	US-09-733-507-8	Sequence 8, Appli
4	122	19.5	642	18	US-10-451-139-8	Sequence 8, Appli
5	50.2	8.0	1040	18	US-10-424-599-69339	Sequence 69339, A
6	48.8	7.8	1261	18	US-10-424-599-67348	Sequence 67348, A
7	47.2	7.5	1237	18	US-10-424-599-40086	Sequence 40086, A

RESULT 1

US-09-733-507-7  
; Sequence 7, Application US/09733507  
; Patent No. US20010025379A1  
; GENERAL INFORMATION:  
; APPLICANT: Agriculture and Agri-Food Canada; The University of Saskatchewan  
; TITLE OF INVENTION: Cyclin Dependent Kinase Inhibitors as Plant Growth  
; TITLE OF INVENTION: Regulators  
; FILE REFERENCE: 81601-3  
; CURRENT APPLICATION NUMBER: US/09/733,507  
; CURRENT FILING DATE: 2000-12-02  
; PRIOR APPLICATION NUMBER: CA 2,256,121  
; PRIOR FILING DATE: 1998-12-31  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-733-507-7

Query Match	97.9%	Score	612.8	DB 9	Length	824
Best Local Similarity	99.7%	Pred. No.	3.7e-181			
Matches	614	Conservative	0	Mismatches	2	Indels
						Gaps
						0
QY	11	ACCCAAAATCCAGAGAGAAAAAATGAGCCGAGAGAAAGCGAGAGCTTCGAGAAGC	70			
Db	24	ACACAAAATCCAGAGAGAAAAAATGAGCCGAGAGAAAGCGAGAGCTTCGAGAAGC	83			
QY	71	TTCAAGCACAGCTTCTCACCACTGAAAGAAACGAAAGCTTAATGATTCTTCTGATTCTATC	130			



Db 213 ATCTGAAGAAGAGCGATCATCTAAGCTCAAGCATCAGCTCTGGTTGTTCCAGCAGCA 272  
Qy 281 ATCGAAGAAATCGGAAGAACAGTTTCGTTGGTGTAGATCTGGAGGATCATCAAT 340  
Db 273 AACTAAGAAATCGCTACTCGTCTTCCATTTTC-----AGATCTGGAGGCTCATGAAAT 326  
Qy 341 CGAAACCGAAACCGAAACCTCAACATTCATCACCAGCAATTTTCAGAAAGAGACAGATCC 400  
Db 327 CT---CCGAAACCGAAATCTCAACGTTTACTCACCACAAATTTTCAGGAAACAGGGAAATTTTC 383  
Qy 401 AGTGAGTGAAGGTTTGGGAGAAACGACAAAGAAATGGAATCATCATCGGCAACGAGAG 460  
Db 384 ATCAAGCGAGAAATCTGGAGAA---ACAGCAGAAATGGAATCGGCGACGACGAGATGAG 440  
Qy 461 AAAACAACCGGGGTGAGGAAGA-----CTCAAACGGCGCGGAGAT 502  
Db 441 AGATCAGAGAAAGACGGAGAAAGAAAGATGGAATAATCACCAGCGCAGGAGAGCT 500  
Qy 503 TGAGGATTTGTTCTGGAGCTAGAGATCCAGACGATAGAAGAACCAATTCATAGAAAA 562  
Db 501 TGATGACTTTTCTCGCGCGCGGAGAG-----ATACGAAACAGAAACGATTCACAGAAAA 554  
Qy 563 GTACAACCTTCGATATTGTCAATGACGAACCGCTTCAAGGTCTGCTACAAGTGGGATCGACT 622  
Db 555 GTACAACCTACGACATCGTCAATGATACCGCGCTTGAAGTCCGTACCGTGGGTAGTCT 614  
Qy 623 TTAA 626  
Db 615 GAAA 618

## RESULT 4

US-10-451-139-8  
; Sequence 8, Application US/10451139  
; Publication No. US20040098763A1  
; GENERAL INFORMATION:  
; APPLICANT: WANG, HONG  
; APPLICANT: ZHOU, YONGMING  
; APPLICANT: FOWKE, LARRY C.  
; APPLICANT: HER MAJESTY IN RIGHT OF CANADA AS REPRESENTED BY THE MINISTER OF  
; APPLICANT: AGRICULTURE AND AGRIFOOD CANADA  
; TITLE OF INVENTION: MODULATION OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR  
; FILE REFERENCE: 4810-62237  
; CURRENT APPLICATION NUMBER: US/10/451,139  
; CURRENT FILING DATE: 2003-06-18  
; PRIOR APPLICATION NUMBER: WO PCT/CA01/01825  
; PRIOR FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: US 60/255,908  
; PRIOR FILING DATE: 2000-12-18  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 642  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-10-451-139-8

Query Match 19.5%; Score 122; DB 18; Length 642;  
Best Local Similarity 63.0%; Pred. No. 2.7e-27;  
Matches 305; Conservative 0; Mismatches 140; Indels 39; Gaps 6;

Qy 164 TTCATCTCTTCGTTGCTTCGTCGGCGGCTTTAGCGTCTGATGATGTTCCGTTACCAT 223  
Db 153 TTCCCTCTCTCTCGCTTACTCGGTTTCAGATTCCGGAGGTTTCTGCTCGTCCGCTT 212  
Qy 224 CGGTGAGAAGAAAGTATCA---GTCTCGAGTATCAGCTCCGGTGTGTTTCCACAGTGA 280  
Db 213 ATCTGAAGAAGAACGATCATCTAAGCTCAAGCATCAGCTCTGGTGTGTTTCCAGCAGCA 272  
Qy 281 ATCGAAGAAATCGGCAAGAACAGTTCGTTGTTGTTAGATCTCGAGGATCATCAAT 340

Db 273 AACTAAGAAATCGCTACTCTCGTCTTCCATTTTC-----AGATCTGGAGGCTCATGAAAT 326  
Qy 341 CGAAACCGAAACCGAAACCTCAACATTCATCACCAGCAATTTTCAGAAAGAGACAGATCC 400  
Db 327 CT---CCGAAACCGAAATCTCAACGTTTACTCACCACAAATTTTCAGGAAACAGGGAAATTTTC 383  
Qy 401 AGTGAGTGAAGGTTTGGGAGAAACGACAAAGAAATGGAATCATCATCGGCAACGAGAG 460  
Db 384 ATCAAGCGAGAAATCTGGAGAA---ACAGCAGAAATGGAATCGGCGACGACGAGATGAG 440  
Qy 461 AAAACAACCGGGGTGAGGAAGA-----CTCAAACGGCGCGGAGAT 502  
Db 441 AGATCAGAGAAAGACGGAGAAAGAAAGATGGAATAATCACCAGCGCAGGAGAGCT 500  
Qy 503 TGAGGATTTGTTCTGGAGCTAGAGATCCAGACGATAGAAGAACCAATTCATAGAAAA 562  
Db 501 TGATGACTTTTCTCGCGCGCGGAGAG-----ATACGAAACAGAAACGATTCACAGAAAA 554  
Qy 563 GTACAACCTTCGATATTGTCAATGACGAACCGCTTCAAGGTCTGCTACAAGTGGGATCGACT 622  
Db 555 GTACAACCTACGACATCGTCAATGATACCGCGCTTGAAGTCCGTACCGTGGGTAGTCT 614  
Qy 623 TTAA 626  
Db 615 GAAA 618

## RESULT 5

US-10-424-599-69339  
; Sequence 69339, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 69339  
; LENGTH: 1040  
; TYPE: DNA  
; ORGANISM: Glycine max  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_33625C.1  
US-10-424-599-69339

Query Match 8.0%; Score 50.2; DB 18; Length 1040;  
Best Local Similarity 65.2%; Pred. No. 0.00012;  
Matches 92; Conservative 0; Mismatches 43; Indels 6; Gaps 1;

Qy 479 GAAGACTCCACGGCGCGGAGATTGAGGATTTGTTCTCGGAGCTAGAGAGTCCAGACGA 538  
Db 447 GAAGACGCCACCACAGCAGAGATCGAAGAGTTTTTCGGCATGGCGGA-----AAAGTA 500  
Qy 539 TAAGAAGAACCAATTCATAGAAAAGTACAACCTTCGATATTGTCAATGACGAACCGCTTGA 598  
Db 501 CGAGCGAAAACGGTTTCACAGAGAAGTACAACCTTCGATATTGTAGAGATTTCCCGTTGGA 560  
Qy 599 AGGTCTGCTACAGTGGGATCG 619  
Db 561 GGGTCGCTACCAAGTGGGTTTCG 581

## RESULT 6

US-10-424-599-67348  
; Sequence 67348, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J

```

; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 92958
; LENGTH: 1360
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_54958C.1
US-10-424-599-92958

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	Query Match	7.58;	Score 47.2;	DB 18;	Length 1360;
	Best Local Similarity	63.08;	Pred. No. 0.0012;		
	Matches 92;	Conservative 0;	Mismatches 48;	Indels 6;	Gaps 1
QY	477	AGGAAGACTCCAACGGCGGAGATTGAGAGATTGTCTCGGAGCTAGAGAGTCCAGAC	536		
Db	575	AGAAACATTCCAACGGCTTATGAGATGGAGAGTCTTGTGTTATCGCGAGA-----AG	628		
QY	537	GATAAGAAGAAGCAAAATTCATAGAAAAAGTCAAACTTCGATATTGTCAATGACGAACCGGTT	596		
Db	629	CAGCAACAACAATATTATGGACAAAGTCAAAATTTCCACATTGTCAATGAAGTACCTCTG	688		
QY	597	GAAGGTCGTACAAGTGGGATCGACT	622		
Db	689	CCTGGACGGTACAGTGGGTCCAGT	714		

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RESULT 9
US-09-733-507-15
; Sequence 15, Application US/09733507
; Patent No. US20010025379A1
; GENERAL INFORMATION:
; APPLICANT: Agriculture and Agri-Food Canada; The University of Saskatchewan
; TITLE OF INVENTION: Cyclin Dependant Kinase Inhibitors as Plant Growth
; TITLE OF INVENTION: Regulators
; FILE REFERENCE: 81601-3
; CURRENT APPLICATION NUMBER: US/09/733,507
; CURRENT FILING DATE: 2000-12-02
; PRIOR APPLICATION NUMBER: CA 2,256,121
; PRIOR FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 804
; TYPE: DNA
; ORGANISM: Chenopodium rubrum
US-09-733-507-15

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	Query Match	7.4%;	Score 46.2;	DB 9;	Length 804;	
	Best Local Similarity	59.2%;	Pred. No. 0.0018;			
	Matches 100;	Conservative	0;	Mismatches 63;	Indels 6;	Gaps 1
QY	454	CGAAGAGAAACACCGGGGGTGGAGGAAGACTCCACGGCGGGGAGAGATTGAGGATTGT	513			
Db	476	CGGCGACGAAATCAACGGTACAGATCAAGATGCCGTCTGATTACAGAAATCGAAGAATTCT	535			
QY	514	TCTCGGAGCTAGAGAGTCCAGACGATAAGAAGCAATTCATAGAAAAAGTACAACTTCG	573			
Db	536	TTGCTGTGCTGA-----AAAAGATCTCCAGAAACGCTTCAGCGAAAAGTACAAATTCG	589			
QY	574	ATATTGTCATGACGAACCGCTTGAAGGTCCGCTCAAGTCGGATCGACT	622			
Db	590	ACATAGTTAAGGACGTGCCACTGAAGGTCGTTATGATTGGGTTCCTCAAT	638			

QY	574	ATATTGTCAAATGACGAACCGCTTGAAGTTCGCTCAAGTGGATCGACT	622
Db	590	ACATAGTTAAGGACGTCGCCACTGAAGGTCGTTATGATTGGTTCCAAT	638
RESULT 10			
US-10-451-139-14			

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; Sequence 14, Application US/10451139
; Publication No. US20040098763A1
; GENERAL INFORMATION:
; APPLICANT: WANG, HONG
; APPLICANT: ZHOU, YONGMING
; APPLICANT: FOWKE, LARRY C.
; APPLICANT: HER MAJESTY IN RIGHT OF CANADA AS REPRESENTED BY THE MINISTER OF
; AGRICULTURE AND AGRI-FOOD CANADA
; TITLE OF INVENTION: MODULATION OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR
; TITLE OF INVENTION: ACTIVITY
; FILE REFERENCE: 4810-62237
; CURRENT APPLICATION NUMBER: US/10/451,139
; PRIOR FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: WO PCT/CA01/01825
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,908
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 804
; TYPE: DNA
; ORGANISM: Chenopodium rubrum
US-10-451-139-14

Query Match          7.4%; Score 46.2; DB 18; Length 804;
Best Local Similarity 59.2%; Pred. No. 0.0018;
Matches 100; Conservative 0; Mismatches 63; Indels 6; Gaps 1;

QY 454 CGAAGAGAAACAAACCGGGGTGAGGAAGACTCCAAACGGCGGAGATTGAGGATTTGCT 513
DB 476 CGCGAGAGAAATCAACGGTACAGATCAAGATCGCTGCTGATTCAGAAATCGAAGATTC 535
QY 514 TTCGGAGCTAGAGAGCTCAGACGATAGAGAAAGCAATTCATAGAAAAGTACAACTTCG 573
DB 536 TTGCTGTTGCTGA-----AAAAGATCTCCAGAAACGCTTCAGCGAAAAGTACAAATTCG 589
QY 574 ATATTGTCATGACGAACCGCTTGAAGTTCGCTACAAAGTGGGATCGAAT 622
DB 590 ACATAGTTAAGGACGTCGCACTGAAAGGTCGTTATGATTTGGGTTCCAAT 638

RESULT 11
US-09-733-507-5
; Sequence 5, Application US/09733507
; Patent No. US20010025379A1
; GENERAL INFORMATION:
; APPLICANT: Agriculture and Agri-Food Canada; The University of Saskatchewan
; TITLE OF INVENTION: Cyclin Dependant Kinase Inhibitors as Plant Growth
; TITLE OF INVENTION: Regulators
; FILE REFERENCE: 81601-3
; CURRENT APPLICATION NUMBER: US/09/733,507
; PRIOR FILING DATE: 2000-12-02
; PRIOR APPLICATION NUMBER: CA 2,256,121
; PRIOR FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 377
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-733-507-5

Query Match          7.3%; Score 45.8; DB 9; Length 377;
Best Local Similarity 62.9%; Pred. No. 0.0016;
Matches 90; Conservative 0; Mismatches 47; Indels 6; Gaps 1;

QY 473 GGTGAGGAAGACTCCAAACGGCGGAGATTGAGGATTTGTTCTCGAGCTAGAGAGTCC 532
DB 181 GATGACGGAGATGCCACCGAATCGGAATTCGAAGATTTTGTGGAAGCTGAGAAACA 240
QY 533 AGACGATAGAAAGCAATTCATAGAAAAGTACAACTTCGATATTTGTCATGACGAACC 592
DB 241 ACTC-----AAAGAAAATTCAGAAGAAAGTACAATTCGATTTCCGAGAGGAGAGGCC 294
QY 593 GCTTGAAGGTCGCTCAAGTGGG 615
DB 295 ATTAGAAGGACGTTACGAATGGG 317

RESULT 13
US-09-733-507-4
; Sequence 4, Application US/09733507
; Patent No. US20010025379A1
; GENERAL INFORMATION:
; APPLICANT: Agriculture and Agri-Food Canada; The University of Saskatchewan
; TITLE OF INVENTION: Cyclin Dependant Kinase Inhibitors as Plant Growth
; TITLE OF INVENTION: Regulators
; FILE REFERENCE: 81601-3
; CURRENT APPLICATION NUMBER: US/09/733,507
; PRIOR FILING DATE: 2000-12-02
; PRIOR APPLICATION NUMBER: CA 2,256,121
; PRIOR FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 443
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-733-507-4

; Sequence 14, Application US/10451139
; Publication No. US20040098763A1
; GENERAL INFORMATION:
; APPLICANT: WANG, HONG
; APPLICANT: ZHOU, YONGMING
; APPLICANT: FOWKE, LARRY C.
; APPLICANT: HER MAJESTY IN RIGHT OF CANADA AS REPRESENTED BY THE MINISTER OF
; AGRICULTURE AND AGRI-FOOD CANADA
; TITLE OF INVENTION: MODULATION OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR
; TITLE OF INVENTION: ACTIVITY
; FILE REFERENCE: 4810-62237
; CURRENT APPLICATION NUMBER: US/10/451,139
; PRIOR FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: WO PCT/CA01/01825
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,908
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 377
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Sequence: alternative cDNA iCK1b
US-10-451-139-4

Query Match          7.3%; Score 45.8; DB 18; Length 377;
Best Local Similarity 62.9%; Pred. No. 0.0016;
Matches 90; Conservative 0; Mismatches 47; Indels 6; Gaps 1;

QY 473 GGTGAGGAAGACTCCAAACGGCGGAGATTGAGGATTTGTTCTCGAGCTAGAGAGTCC 532
DB 181 GATGACGGAGATGCCACCGAATCGGAATTCGAAGATTTTGTGGAAGCTGAGAAACA 240
QY 533 AGACGATAGAAAGCAATTCATAGAAAAGTACAACTTCGATATTTGTCATGACGAACC 592
DB 241 ACTC-----AAAGAAAATTCAGAAGAAAGTACAATTCGATTTCCGAGAGGAGAGGCC 294
QY 593 GCTTGAAGGTCGCTCAAGTGGG 615
DB 295 ATTAGAAGGACGTTACGAATGGG 317

RESULT 12
US-10-451-139-4
; Sequence 4, Application US/10451139
; Publication No. US20040098763A1
; GENERAL INFORMATION:
; APPLICANT: WANG, HONG
; APPLICANT: ZHOU, YONGMING
; APPLICANT: FOWKE, LARRY C.
; APPLICANT: HER MAJESTY IN RIGHT OF CANADA AS REPRESENTED BY THE MINISTER OF
; AGRICULTURE AND AGRI-FOOD CANADA
; TITLE OF INVENTION: MODULATION OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR
; TITLE OF INVENTION: ACTIVITY
; FILE REFERENCE: 4810-62237
; CURRENT APPLICATION NUMBER: US/10/451,139
; PRIOR FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: WO PCT/CA01/01825
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,908
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 377
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Sequence: alternative cDNA iCK1b
US-10-451-139-4

Query Match          7.3%; Score 45.8; DB 18; Length 377;
Best Local Similarity 62.9%; Pred. No. 0.0016;
Matches 90; Conservative 0; Mismatches 47; Indels 6; Gaps 1;

QY 473 GGTGAGGAAGACTCCAAACGGCGGAGATTGAGGATTTGTTCTCGAGCTAGAGAGTCC 532
DB 181 GATGACGGAGATGCCACCGAATCGGAATTCGAAGATTTTGTGGAAGCTGAGAAACA 240
QY 533 AGACGATAGAAAGCAATTCATAGAAAAGTACAACTTCGATATTTGTCATGACGAACC 592
DB 241 ACTC-----AAAGAAAATTCAGAAGAAAGTACAATTCGATTTCCGAGAGGAGAGGCC 294
QY 593 GCTTGAAGGTCGCTCAAGTGGG 615
DB 295 ATTAGAAGGACGTTACGAATGGG 317

RESULT 13
US-09-733-507-4
; Sequence 4, Application US/09733507
; Patent No. US20010025379A1
; GENERAL INFORMATION:
; APPLICANT: Agriculture and Agri-Food Canada; The University of Saskatchewan
; TITLE OF INVENTION: Cyclin Dependant Kinase Inhibitors as Plant Growth
; TITLE OF INVENTION: Regulators
; FILE REFERENCE: 81601-3
; CURRENT APPLICATION NUMBER: US/09/733,507
; PRIOR FILING DATE: 2000-12-02
; PRIOR APPLICATION NUMBER: CA 2,256,121
; PRIOR FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 443
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-733-507-4
```

```

Query Match      7.3%; Score 45.8; DB 9; Length 443;
Best Local Similarity 62.9%; Pred. No. 0.0018;
Matches 90; Conservative 0; Mismatches 47; Indels 6; Gaps 1;

QY 473 GGTGAGGAAGACTCCAAACGGCGGAGATTGAGGATTTGTTCTCGGAGCTAGAGAGTCC 532
Db 199 GATGACGAGATGCCAACGGAAATCGGAATTTGTTGTTGGAAGCTGAGAAACA 258

QY 533 AGACGATAAGAGAGCAATTCATAGAAAAGTACAACTTCGATATTGTCAATGACGAACC 592
Db 259 ACTC-----AAAGAAAATTCAAGAGAAGTACAAATTCGATTTCGAGAAGGAGAAGCC 312

QY 593 GCTTGAAGTCGCTACAAGTGGG 615
Db 313 ATTAGAAGGACGTTACGAATGGG 335

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RESULT 14
US-10-451-139-5
; Sequence 5, Application US/104511139
; Publication No. US20040098763A1
; GENERAL INFORMATION:
; APPLICANT: WANG, HONG
; APPLICANT: ZHOU, YONGMING
; APPLICANT: FOWKE, LARRY C.
; APPLICANT: HER MAJESTY IN RIGHT OF CANADA AS REPRESENTED BY THE MINISTER OF
; APPLICANT: AGRICULTURE AND AGRIFOOD CANADA
; TITLE OF INVENTION: MODULATION OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR
; TITLE OF INVENTION: ACTIVITY
; FILE REFERENCE: 4810-62237
; CURRENT APPLICATION NUMBER: US/10/451,139
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: WO PCT/CA01/01825
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,908
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 443
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Sequence: alternative cDNA iCK1c
US-10-451-139-5

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Query Match      7.3%; Score 45.8; DB 18; Length 443;
Best Local Similarity 62.9%; Pred. No. 0.0018;
Matches 90; Conservative 0; Mismatches 47; Indels 6; Gaps 1;

QY 473 GGTGAGGAAGACTCCAAACGGCGGAGATTGAGGATTTGTTCTCGGAGCTAGAGAGTCC 532
Db 199 GATGACGAGATGCCAACGGAAATCGGAATTTGTTGTTGGAAGCTGAGAAACA 258

QY 533 AGACGATAAGAGAGCAATTCATAGAAAAGTACAACTTCGATATTGTCAATGACGAACC 592
Db 259 ACTC-----AAAGAAAATTCAAGAGAAGTACAAATTCGATTTCGAGAAGGAGAAGCC 312

QY 593 GCTTGAAGTCGCTACAAGTGGG 615
Db 313 ATTAGAAGGACGTTACGAATGGG 335

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RESULT 15
US-09-733-507-3
; Sequence 3, Application US/09733507
; Patent No. US20010025379A1
; GENERAL INFORMATION:
; APPLICANT: Agriculture and Agri-Food Canada; The University of Saskatchewan
; TITLE OF INVENTION: Cyclin Dependant Kinase Inhibitors as Plant Growth
; TITLE OF INVENTION: Regulators
; FILE REFERENCE: 81601-3

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; CURRENT APPLICATION NUMBER: US/09/733,507
; CURRENT FILING DATE: 2000-12-02
; PRIOR APPLICATION NUMBER: CA 2,256,121
; PRIOR FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 660
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-733-507-3

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Query Match      7.3%; Score 45.8; DB 9; Length 660;
Best Local Similarity 62.9%; Pred. No. 0.0022;
Matches 90; Conservative 0; Mismatches 47; Indels 6; Gaps 1;

QY 473 GGTGAGGAAGACTCCAAACGGCGGAGATTGAGGATTTGTTCTCGGAGCTAGAGAGTCC 532
Db 372 GATGACGAGATGCCAACGGAAATCGGAATTTGTTGTTGGAAGCTGAGAAACA 431

QY 533 AGACGATAAGAGAGCAATTCATAGAAAAGTACAACTTCGATATTGTCAATGACGAACC 592
Db 432 ACTC-----AAAGAAAATTCAAGAGAAGTACAAATTCGATTTCGAGAAGGAGAAGCC 485

QY 593 GCTTGAAGTCGCTACAAGTGGG 615
Db 486 ATTAGAAGGACGTTACGAATGGG 508

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Search completed: September 30, 2005, 10:44:35  
Job time : 2174 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 30, 2005, 09:05:52 ; Search time 2871 Seconds  
(without alignments)  
8299.628 Million cell updates/sec

Title: US-09-980-758A-7  
Perfect score: 626  
Sequence: 1 ctctagatttccccaaaaa.....acaagtggatcgacttta 626

Scoring table: GAPOT 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*

1: gb\_est1: \*  
2: gb\_est2: \*  
3: gb\_hic: \*  
4: gb\_est3: \*  
5: \* gb\_est4: \*  
6: gb\_est5: \*  
7: gb\_est6: \*  
8: gb\_gssi: \*  
9: gb\_gss2: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	611.4	97.7	797	3	CNS0A7OL
2	605	96.6	893	3	CNS0A6HI
3	585.6	93.5	664	1	AU237797
4	549.4	87.8	736	3	CNS0A5EV
5	527.8	84.3	784	3	CNS0A6Q
6	299.8	47.9	457	5	EX840619
7	214.2	34.2	425	1	AU228889
8	103.2	16.5	408	5	BP670981
9	96.4	15.4	654	8	BZ426940
10	96.4	15.4	831	8	BH708120
11	95.6	15.3	700	8	BZ083701
12	70.4	11.2	747	7	CO408371
13	70.4	11.2	747	7	CO408372
14	70	11.2	712	7	CV234322
15	70	11.2	919	7	CV242992
16	69.2	11.1	197	8	BZ770063
17	64.2	10.3	1017	5	BO481784
18	60	9.6	774	7	CF212022
19	60	9.6	794	6	CF288800
20	60	9.6	888	7	CF212120
21	58.4	9.3	902	5	BO794660
22	55	8.8	682	7	CO980060
23	53	8.5	672	7	CO98695
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27	52.2	8.3	646	6	CD829320	CD829320	BN40.041M
28	51.6	8.2	646	1	A1728644	BNLGH112	
C 29	51.2	8.2	780	7	CV227354	WS0166.B2	
C 30	51.2	8.2	910	7	CV280549	WS0136.B2	
C 31	50.6	8.1	589	1	AV767700	AV767700	
C 32	50.6	8.1	722	7	CO070046	CO070046	GR_E3260
C 33	50.6	8.1	777	7	CO079308	CO079308	GR_E342A
C 34	50.6	8.1	815	7	CO079309	GR_E342A	
C 35	49.6	7.9	945	7	CV280994	WS0138.B2	
C 36	49.4	7.9	595	7	CV296057	EST884434	
C 37	49	7.8	580	7	CK096447	UB14CPG11	
C 38	48.8	7.8	573	6	CD396199	Gm_CK1643	
C 39	48.8	7.8	733	7	CO981606	GW89011B2	
C 40	48.6	7.8	817	7	CK934305	CGF100426	
C 41	48.6	7.8	846	7	CK934861	CGF100422	
C 42	48.6	7.8	997	9	CNS005TE	AL060767	Drosoph11
C 43	48.4	7.7	838	7	CO478922	GQ0178.B7	
C 44	48.2	7.7	602	5	BQ863066	QGC22002	
C 45	47.8	7.6	625	5	BU011062	OGJ15D05	

## ALIGNMENTS

RESULT 1  
CNS0A7OL 797 bp mRNA linear HTC 06-FEB-2004  
LOCUS Arabidopsis thaliana Full-length cDNA Complete sequence from clone  
DEFINITION GSLTSL92E05 of Silique of strain col-0 of Arabidopsis thaliana  
(thale cress).

ACCESSION BX826283  
VERSION BX826283.1 GI:42466833

KEYWORDS HTC; GSLT cDNA.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE 1 (bases 1 to 797)

AUTHORS

Castelli, V., Aury, J.M., Jallou, O., Wincker, P., Clepet, C.,  
Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V.,  
Temple, G., Caboche, M., Weissenbach, J., and Salanoubat, M.

Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:  
A Combined Approach to Evaluate and Improve Arabidopsis Genome

Annotation

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 797)

AUTHORS Genoscope.

JOURNAL Direct Submission

Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)

COMMENT

The sequences are based on single pass reads.  
Life Technologies (a division of Invitrogen) members carried out  
full-length libraries construction : Temple G.

Genoscope members carried out sequencing and annotation : Castelli  
V., Aury J.M., Jallou O., Wincker P., Menard M., Cruaud C.,  
Schachter V., Weissenbach J., Salanoubat M.

URGV INRA : Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis  
genome released by MIPS (Munich Information center for Protein  
Sequences) . 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque\_Projet\_EF/Full  
length

http://www.genoscope.cns.fr/cgi-bin/ggb?source=Arabidopsis.  
Location/Qualifiers

FEATURES

source

1..797  
/organism="Arabidopsis thaliana"  
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Qy	74	AAGCACAAGCTTCTCACCACCTGAGAAACGAAAGCTTAATGATCTTCTGATTCATCAC	133
Db	61	AAGCACAAGCTTCTCACCACCTGAGAAACGAAAGCTTAATGATCTTCTGATTCATCAC	120
Qy	134	GGACTCTCATGACGTCATCGTCTTCGCGGTTTCATCTTCTCCGTTGCTTCGTCGGCGGC	193
Db	121	GGACTCTCATGACGTCATCGTCTTCGCGGTTTCATCTTCTCCGTTGCTTCGTCGGCGGC	180
Qy	194	TTTAGCGTCTGATGAATGTTCCGTTTACCATTCCGTTGAGAGAAAGTGAATCCTCGAG	253
Db	181	TTTAGCGTCTGATGAATGTTCCGTTTACCATTCCGTTGAGAGAAAGTGAATCCTCGAG	240
Qy	254	TATCAGCTCCGGTTGTTTCCAGCTGAATCGAAGAAATCGGAAGAACAGTTCGTCGTT	313
Db	241	TATCAGCTCCGGTTGTTTCCAGCTGAATCGAAGAAATCGGAAGAACAGTTCGTCGTT	300
Qy	314	TGGTGTAGATCTGAGAGATCATCAATCGAAACCGAAACCGAAACCGAAACCGAAACCG	373
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Db	361	CAGCAATTCAGAAAAGAGACAGTCCAGTGAAGTGGAGTGGAGTGGAGTGGAGTGGAGT	420
Qy	434	AATGGAATCATCATCGGCAACGAGAGAAACACACCGGGGTGAGGAGACTCCAAACGCG	493
Db	421	AATGGAATCATCATCGGCAACGAGAGAAACACACCGGGGTGAGGAGACTCCAAACGCG	480
TITLE		Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation	
JOURNAL REFERENCE		Unpublished 2 (bases 1 to 893) Genoscope. Direct Submission Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)	
AUTHORS		The sequences are based on single pass reads. Life Technologies (a division of Invitrogen) members carried out full-length libraries construction : Temple G. Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M. URGV INRA : Clepet C., Caboche M. Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap. http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full _length http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.	
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JOURNAL		source	
COMMENT		gene	
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Db	1	CAAAATCCAAAGAGAGAAAAAATGAGCGAGAGAAAGCGAGAGCTTGCAGAAAGACTTC	60
Qy	74	AAGCACAAGCTTCTCACCACCTGAAGAAAACGAAAGCTTAATGATCTTCTGATTCATCAC	133
Db	61	AAGCACAAGCTTCTCACCACCTGAAGAAAACGAAAGCTTAATGATCTTCTGATTCATCAC	120
Qy	134	GGACTCTCATGACGTCATCGTCTTCGCGGTTTCATCTTCTCCGTTGCTTCGTCGGCGGC	193
Db	121	GGACTCTCATGACGTCATCGTCTTCGCGGTTTCATCTTCTCCGTTGCTTCGTCGGCGGC	180
Qy	194	TTTAGCGTCTGATGAATGTTCCGTTTACCATTCCGTTGAGAGAAAGTGAATCCTCGAG	253
Db	181	TTTAGCGTCTGATGAATGTTCCGTTTACCATTCCGTTGAGAGAAAGTGAATCCTCGAG	240
Qy	254	TATCAGCTCCGGTTGTTTCCAGCTGAATCGAAGAAATCGGAAGAACAGTTCGTCGTT	313
Db	241	TATCAGCTCCGGTTGTTTCCAGCTGAATCGAAGAAATCGGAAGAACAGTTCGTCGTT	300
Qy	314	TGGTGTAGATCTGAGAGATCATCAATCGAAACCGAAACCGAAACCGAAACCGAAACCG	373
Db	301	TGGTGTAGATCTGAGAGATCATCAATCGAAACCGAAACCGAAACCGAAACCGAAACCG	360
Qy	374	CAGCAATTCAGAAAAGAGACAGTCCAGTGAAGTGGAGTGGAGTGGAGTGGAGTGGAGT	433
Db	361	CAGCAATTCAGAAAAGAGACAGTCCAGTGAAGTGGAGTGGAGTGGAGTGGAGTGGAGT	420
Qy	434	AATGGAATCATCATCGGCAACGAGAGAAACACACCGGGGTGAGGAGACTCCAAACGCG	493
Db	421	AATGGAATCATCATCGGCAACGAGAGAAACACACCGGGGTGAGGAGACTCCAAACGCG	480
Qy	494	GGCGAGATTCGAGGATTTGTTCTCGAGCTAGAGAGTCCAGACGATAGAGAGAGCAATT	553
Db	481	GGCGAGATTCGAGGATTTGTTCTCGAGCTAGAGAGTCCAGACGATAGAGAGAGCAATT	540
Qy	554	CATGAAAAGTACAACTTCGATATTGTCAATGACGAACCGCTTGAAGGTGCGTCAAGTG	613
Db	541	CATGAAAAGTACAACTTCGATATTGTCAATGACGAACCGCTTGAAGGTGCGTCAAGTG	600
Qy	614	GGATCGACTTTAA 626	
Db	601	GGATCGACTTTAA 613	
RESULT 2		CN50A6HI 893 bp mRNA linear HTC 06-FEB-2004	
LOCUS		Arabidopsis thaliana Full-length cDNA Complete sequence from clone	
DEFINITION		GSLTSIL21ZF04 of Silique of strain col-0 of Arabidopsis thaliana (thale cress).	
ACCESSION		BX825232	
VERSION		BX825232.1 GI:42465135	
KEYWORDS		HTC; GSLT_cDNA.	
SOURCE		Arabidopsis thaliana (thale cress)	
ORGANISM		Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicaceae; Arabidopsis.	
REFERENCE		1 (bases 1 to 893) Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C., Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,	
AUTHORS			

QY 494 GCGGAGATTGAGGATTTCTCGAGCTAGAGAGTCCAGACGATAGAAAGCAATT 553  
 DB 481 GCGGAGATTGAGGATTTCTCGAGCTAGAGAGTCCAGACGATAGAAAGCAATT 540  
 QY 554 CATAGAAAAGTACAACTTCGATATTGTCAATGACCAACCGCTTGAAGGTCGCTACAAGTG 613  
 DB 541 CATAGAAAAGTACAACTTCGATATTGTCAATGACCAACCGCTTGAAGGTCGCTACAAGTG 600  
 QY 614 GGATCGACTTTAA 626  
 DB 601 GGATCGACTTTAA 613

RESULT 3  
 AU237797  
 LOCUS AU237797 RAF16 Arabidopsis thaliana cDNA clone RAPL16-57-G19 5',  
 DEFINITION mRNA sequence.

ACCESSION AU237797  
 VERSION AU237797.1 GI:19876966  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 664)  
 Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,  
 Akiyama, K., Enju, A., Oono, Y., Sakurai, T., Carninci, P., Kawai, J.,  
 Itoh, M., Tahii, Y., Arakawa, T., Shibata, K., Shinagawa, A.,  
 Muramatsu, M., Hayashizaki, Y., and Shinozaki, K.  
 Large scale analysis of Arabidopsis full-length cDNA  
 Unpublished (2002)  
 Contact: Motoaki Seki

PLANT Functional Genomics Research Group  
 RIKEN Genomic Sciences Center  
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
 Tel: 81-298-36-4359  
 Fax: 81-298-36-9060  
 Email: mseki@rtc.riken.go.jp

An Arabidopsis full-length cDNA library was constructed essentially  
 as reported previously (Seki et al., 1998) cDNA cleaved with BamHI  
 and XhoI was ligated to modified lambda FLC-1 vector (Carninci et  
 al., submitted for publication) digested with BamHI and SalI. This  
 clone is in a modified pBluescript vector. Please visit our web  
 site ([http://www.gsc.riken.go.jp/e/plant/index\\_e.html](http://www.gsc.riken.go.jp/e/plant/index_e.html)) for further  
 details.

FEATURES  
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ORIGIN  
 Query Match 93.5%; Score 585.6; DB 1; Length 664;  
 Best Local Similarity 97.9%; Pred. NO. 2.6e-160;  
 Matches 602; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

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 DB 16 ACACAAAATCCAGAGAGAAAAATGAGCGAGAGAAAGCGAGCTTGACAGAGAGC 75  
 QY 71 TTCAGCAACAGTTCTCCACCTGAAGAAACGAAGCTTAATGATTTCTGATTCATC 130  
 DB 76 TTCAGCAACAGTTCTCCACCTGAAGAAACGAAGCTTAATGATTTCTGATTCATC 135  
 QY 131 ACCGAGCTTCATGAGTCATCGTCTTCGGGTTTCATCTTCTCGTTGCTTCGTCGC 190  
 DB 136 ACCGAGCTTCATGAGTCATCGTCTTCGGGTTTCATCTTCTCGTTGCTTCGTCGC 195

QY 191 GCCTTTAGCTCTGATGATGTTCCGTTACCATCGGTGAGAGAAAGTATCAGTCTCTC 250  
 DB 196 GCCTTTAGCTCTGATGATGTTCCGTTACCATCGGTGAGAGAAAGTATCAGTCTCTC 255  
 QY 251 GAGTATCAGTCCGGTGTGTTCCACAGTGAATCGAAAGAAATCGGAGAAACAGATTCGTC 310  
 DB 256 GAGTATCAGTCCGGTGTGTTCCACAGTGAATCGAAAGAAATCGGAGAAACAGATTCGTC 315  
 QY 311 GTTGGTGTAGATCTGGAGGATCATCAATCGAAACCGAAACCTCAACATTCAT 370  
 DB 316 GTTGGTGTAGATCTGGAGGATCATCAATCGAAACCGAAACCTCAACATTCAT 375  
 QY 371 CACGAGCAATTCAGAAAAGAGACAGTCCAGTGAAGGTTTGGGAGAAACGACAAC 430  
 DB 376 CACGAGCAATTCAGAAAAGAGACAGTCCAGTGAAGGTTTGGGAGAAACGACAAC 435  
 QY 431 AGAAATGAATCATCATCGCAACGAAGAGAAACCAACCGGGGTGAGGAGACTCCAAAC 490  
 DB 436 AGAAATGAATCATCATCGCAACGAAGAGAAACCAACCGGGGTGAGGAGACTCCAAAC 495  
 QY 491 GCGCGCGAGATTGAGGATTTTCTCGGAGCTAGAGATCCAGACGATTAAGAAGCA 550  
 DB 496 GCGCGCGAGATTGAGGATTTTCTCGGAGCTAGAGATCAAGACGATNAGAAGCA 555  
 QY 551 ATTCATAGAAAAGTACACTTCGATATTGTCAATCAGAACCGCTTGAAGGTCGTACAA 610  
 DB 556 ATTCATAGAAAAGT-CCAATTCGATATTGNCATCAACCAACCGCTTGAAGGTCGTCCAG 614  
 QY 611 GTGGGATCGACTTTA 625  
 DB 615 TGGGATCGACTTTA 629

## RESULT 4

CNS0A6EV  
 LOCUS CNS0A6EV  
 DEFINITION Arabidopsis thaliana Full-length cDNA Complete sequence from clone  
 GSLSIL872B03 of Silique of strain col-0 of Arabidopsis thaliana  
 (thale cress).

ACCESSION BX826140  
 VERSION BX826140.1 GI:42465305  
 KEYWORDS HTC; GSLT\_cDNA  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 736)  
 Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C.,  
 Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V.,  
 Temple, G., Caboche, M., Weissenbach, J., and Salanoubat, M.  
 Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:  
 A Combined Approach to Evaluate and Improve Arabidopsis Genome  
 Annotation

JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 736)  
 Genoscope.  
 Direct Submission  
 Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :  
 BP 191 91006 EVRY cedex - FRANCE [E-mail : seqref@genoscope.cns.fr  
 - Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)]

The sequences are based on single pass reads.  
 Life Technologies (a division of Invitrogen)  
 full-length libraries construction : Temple G.  
 Genoscope members carried out sequencing and annotation : Castelli  
 V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,  
 Schachter V., Weissenbach J., Salanoubat M.

URV INRA : Clepet C., Caboche M.  
 Annotation is based on the June 2003 version of the Arabidopsis  
 genome released by MIPS (Munich Information center for Protein  
 Sequences). 5 prime and 3 prime are assembled with Phrap.  
[http://www.genoscope.cns.fr/externe/sequences/Banque\\_Projet\\_RF/Full](http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_RF/Full)



QY 430 CAGAAATGGAT-CATCATCGG-CAACGAGAGAAAACACCGGGGTGAGGAGACTCC 487  
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 Db 421 CAGAAATGGATGCATCGCGCAACGAGAGAAAACACCGGGGTGAGGAGACTCC 480  
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 QY 488 AACGGCGCGGAGATTGAGGATTTGTTCTCGGAGCTAGAGAGTCCAGACGATAGAAGAA 547  
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 Db 481 AACGGCGCGGAGATTGAGGATTTGTTCTCGGAGCTAAGAGTCAAGACGATAGAAGAA 540  
 |||||  
 QY 548 GCAATTCATAGAAAAGTCAACTTCGATATTGTCAATGACGAACCGCTTGAAGGTCGCTA 607  
 |||||  
 Db 541 GCAATTCATAGAAAAGTCAACTTCGATATTGTCAATGACGAACCGCTTAAAGGTCGCTA 600  
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 QY 608 CAAAGTCGGATCGACTTTAA 626  
 |||||  
 Db 601 CAAAGTCGGATCGACTTTAA 619  
 |||||

RESULT 6  
 BX840619  
 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

REFERENCE  
 AUTHORS  
 TITLE

JOURNAL  
 COMMENT

TITLE  
 JOURNAL  
 COMMENT

FEATURES  
 source

ORIGIN

Query Match  
 Best Local Similarity  
 Matches 373; Conservative 0; Mismatches 22; Indels 10; Gaps 5;  
 QY 29 GAAAAAATGAGCGAGAGAAAGCGAGGCTTCGAGAGAAAGCTTCAAGCACAGGCTTCTC 88  
 |||||  
 Db 1 GAAAAAATGAGCGAGAGAAAGCGAGG- TTGAGAGAAAGCTTCAAGCACAGGCTTCTC 59  
 |||||

QY 89 ACCACTGAAGAAAACGAGCTTAATGATTTCTTCTGATTTATCATCACCGGACTTCTCATGCGT 148  
 |||||  
 Db 60 ACCACTGAAGAAAACGAGCTTAATGATTTCTTCTGATTTATCATCACCGGACTTCTCATGCGT 119  
 |||||  
 QY 149 CATCGTCTTCGCGGTTTTCATCTTCTTCGCTTCGCTCGCGGCTTTAGCGTCTGATGA 208  
 |||||  
 Db 120 CATCGTCTTCGCGGTTTTCATCTTCTTCGCTTCGCTCGCGGCTTTAGCGTCTGATGA 179  
 |||||  
 QY 209 ATGTTCCGTTACCATCGGTGGAGAGAAAGTGCATGATCCTCGAGTATCAGTCTCCGGTTG 268  
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 Db 180 ATGTTCCGTTACCATCGGTGGAGAGAAAGTGCATGATCCTCGAGTATCAGTCTCCGGTTG 239  
 |||||  
 QY 269 TTTTCCAGCTGATCGAAGAAATCGGAGAACAGTTCGTCGTT-TGGTGTAGATCTGG 327  
 |||||  
 Db 240 TTTTCCAGCTGATCGAAGAAATCGGAGAACAGTTCGTCGTT-TGGTGTAGATCTGG 299  
 |||||  
 QY 328 AGGATCATCAAAATCGAAACCGAA--ACCTCAACATTTCA--TCACCAGCAATTT 382  
 |||||  
 Db 300 AGGATCATCAAAATCGAAACCGAAAGAAAGTACACATTCACACACAGCGAATTT 359  
 |||||  
 QY 383 CAGAAAAAGAGAC---GAGTCCAGTGCAGTGGGTTTGGGAGAAAC 424  
 |||||  
 Db 360 CAGAAAAAGAGACAGAGTTTCCAAGTGCAGTCCGCGATAGGATGAAC 404  
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RESULT 7  
 AU228889/c  
 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

FEATURES  
 source

ORIGIN

Query Match  
 Best Local Similarity  
 Matches 238; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

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QY 386 AAAAGAGACGAGTCCAGTGAAGTGGGTTTGGGAGAAACGACACAGAAATGGAATCATC 445
    |||
Db 425 AAAAGAGACGAGTCCATTGAGTGAGGTTTGGGAGAAACGACACAGAAATGGAATCATC 366
QY 446 ATCCGACAGAGAGAAACACACCGGGGTGAGGAGACTCAACGGC-GCGGAGATTG 504
    |||
Db 365 ATCCGCAACGAAAGAGAAACACACCGGGGTGAGGAGACTCAACCGCGGGCGGAGATTG 306
QY 505 AGGATTGTCTTCGGAGCTAGAGAGTCCAGACGATAGAAAGCAATTCATAGAAAAGT 564
    |||
Db 305 AGGATTGTCTTCGGAGCTAGAGAGTCAAGACGATAGAGAGCAATTCATAGAAAAGT 246
QY 565 ACAATTTCGATATGTCATATGACGAAACCGCTTTGAAGTGGTGCATCAA-GTGGGATCGACTT 623
    |||
Db 245 ACAACTTCGATATGTCATATGACGAAACCGCTTTGAAGTGGTGCATCAAAGTGGGATCGACTT 186
QY 624 TAA 626
    |||
Db 185 TAA 183

RESULT 8
LOCUS BP670981/c
DEFINITION BP670981 RAFL21 Arabidopsis thaliana cDNA clone RAFL21-37-F21 3',
    mRNA sequence.
ACCESSION BP670981
VERSION BP670981.1 GI:49322484
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
    rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 408)
AUTHORS Seki,M., Narusaka,M., Kamiya,A., Ishida,J., Satou,M., Sakurai,T.,
    Nakajima,M., Enju,A., Akiyama,K., Oono,Y., Muramatsu,M.,
    Hayashizaki,Y., Kawai,J., Carninci,P., Itoh,M., Ishii,Y.,
    Arakawa,T., Shibata,K., Shinagawa,A. and Shinozaki,K.
TITLE Functional annotation of a full-length Arabidopsis cDNA collection
JOURNAL Science 296 (5565), 141-145 (2002)
MEDLINE 21932900
PUBMED 11910074
COMMENT Contact: Motoaki Seki
    Plant Functional Genomics Research Group
    RIKEN Genomic Sciences Center
    3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
    Tel: 81-298-36-4359
    Fax: 81-298-36-4350
    Email: mseki@tc.riken.go.jp
    reversed clone; please visit our web site
    (http://pfweb.gsc.riken.go.jp/) for further details.

FEATURES
    source
        location/Qualifiers
            1..408
                /organism="Arabidopsis thaliana"
                /mol_type="mRNA"
                /db_xref="taxon:3702"
                /clone="RAFL21-37-F21"
                /lab_host="DH10B"
                /clone_lib="RAFL21"
    /note="Site 1: BamHI; Site 2: SalI; Subtraction Library.
    The sequence was obtained from samples subjected to
    various stress and plant hormones-treated"

ORIGIN
Query Match 16.5%; Score 103.2; DB 5; Length 408;
Best Local Similarity 76.2%; Pred. No. 6.5e-19;
Matches 154; Conservative 0; Mismatches 43; Indels 5; Gaps 2;

QY 425 GACACACAGAAATGGAATCATCATCGGCAACGAAAGAGAAACACCGGGGTGAGGAAGAC 484
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Db 381 GAGAACACACAAATGGAATCATCATCGCCACAGAAAAACACCGGGTGAGAGACTCC 322
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QY 485 TCCAACGCGCGGAGATTGAGGATTTGTTCTCGAGCTAGAGAGTCCAGACGATAAGAA 544
    |||
Db 321 CAC---GCCGCGGAGATTGA-GATTTTTCGAACTAGAGAGTCCAGACCATAGAA 267
QY 545 GAAGCAATTCATAGAAAAGTACAACCTTCGATATTGTCAATGACGAAACCGCTTGAAGGTGG 604
    |||
Db 266 GAAACCAATTCATAGAAAATACCACTTCGATATTGTTCATGACGAAACCCCTTGAAGGTCC 207
QY 605 CTACAAGTGGGATCGACTTTAA 626
    |||
Db 206 CTACAGTGGGATCCACTTTAA 185

RESULT 9
LOCUS BZ426940
DEFINITION BONIN07TR BO_1.6_2_KB_tot Brassica oleracea genomic clone BONIN07,
    genomic survey sequence.
ACCESSION BZ426940
VERSION BZ426940.1 GI:26668452
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
    rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 654)
AUTHORS Town,C.D., Van Aken,S., Uterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other GSSs: BONIN07TF
    Contact: Chris Town
    TIGR
    9712 Medical Center Drive, Rockville, MD 20850, USA.
    Tel: 301-838-3523
    Fax: 301-838-0208
    Email: cdtown@tigr.org
    DNA is from a doubled haploid provided by Tom Osborn.
    Seq primer: TR
    Class: sheared ends.
FEATURES
    source
        location/Qualifiers
            1..654
                /organism="Brassica oleracea"
                /mol_type="genomic DNA"
                /strain="TO1000DH3"
                /db_xref="taxon:3712"
                /clone="BONIN07"
                /clone_lib="BO 1.6 2 KB_tot"
                /note="Vector: pHOS1; Site 1: BstXI; 1.6-2 kb sheared
                total DNA inserted into pHOS1 using BstXI linkers"

ORIGIN
Query Match 15.4%; Score 96.4; DB 8; Length 654;
Best Local Similarity 64.7%; Pred. No. 7.2e-17;
Matches 189; Conservative 0; Mismatches 76; Indels 27; Gaps 2;

QY 54 GAGCTTCAGAGAAGCTTCAAGCACAGCTTCTCACCACCTGAAGAAACGAAGCTTAAT 113
    |||
Db 39 GCGGAGCGCTTGAAGCTCCGAGCGCAAGCGACTCGCAACTCAAGAAAGAAGCTCGAT 98
QY 114 GATTCTTCTGATTCATCACCGGACTCTCATGACGTCTCGTCTTCGCGGTTTCATCTTCT 173
    |||
Db 99 GAT-----GACTCTCATGGCGTCTCTTCTCCTCGGGTTCCTTCTCTCT 140
QY 174 TCCGTTGCTTCGTCGGGGCTTTAGCGTCTGATGAATGTCGTTACCATCGGTGGAGAA 233
    |||
Db 141 TCCGTGGCTTCATCGGATGATTCCTCTCGAGCGCGATGCTCTGTACCTCCGCGGAGAA 200
QY 234 GAAAGTGATCAGTCTCTGAGTATCAGCTCCGGTTGTTTCCACAGTGAATCGAAAGAAATC 293
    |||
Db 201 GACGATGACAGAGCTCGATCATC-----TGTTTCAGCACTGAATCGAACGAATC 251
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Vitaceae; Vitis.

## REFERENCE

1 (bases 1 to 747)

## AUTHORS

Fennell, A. and Mathiason, K.

## TITLE

Expressed sequence tags from Vitis riparia buds

## JOURNAL

Unpublished (2004)

## COMMENT

Contact: Anne Fennell  
Horticulture, Forestry, Landscape and Parks Department  
South Dakota State University  
Northern Plains Biostress Laboratory, Box 2140A, Brookings, SD  
57007-0996, USA

Tel: 605 688 6373

Fax: 605 688 4713

Email: Anne.Fennell@sdstate.edu

Seq primer: PolYT.

## FEATURES

source

Location/Qualifiers  
1..747

/organism="Vitis riparia"

/mol\_type="mRNA"

/db\_xref="taxon:96939"

/clone="VRK512"

/dev\_stage="paradormant"

/lab\_host="DH10B"

/clone\_lib="Vitis riparia bud - VRK"

/note="Organ: bud; Vector: pSport 1; Site 1: SalI; Site 2: NotI; VRK is a cDNA library of Vitis riparia paradormant buds. Compound paradormant buds were collected from actively growing shoots on insect and disease free vines. The directionally oriented library was constructed according to Gibco BRL Superscript Plasmid System for cDNA synthesis and plasmid cloning."

## ORIGIN

Query Match 11.2%; Score 70.4; DB 7; Length 747;

Best Local Similarity 58.9%; Pred. No. 3.1e-09;

Matches 166; Conservative 0; Mismatches 101; Indels 15; Gaps 2;

QY 347 CGAAACCGAAACCTCAACATTCATCCAGCAATTTGAGAAAGAGACGAGTCAGTCGAG 406

Db 497 CGAACTGANAACCTCAAGTATAGCGAGCGGAGGTTTCAGTAGAGACCACTCCAGTCGAG 438

QY 407 TGAG-----GGTTGGGAGAAACGACACAGAAATGGAATCATCATCGGCAACGAA 457

Db 437 CGAGCTCCACGCTGATTTCAGCTGAGATGGAGTCTACGCGAAGACTACAGCGGCCAAACC 378

QY 458 GAGAAAACACCGCGGGGTGAGAAAGACTCCAAAGCGCGGGGAGATTGAGATTGTTCTC 517

Db 377 GCGGCGGAAATCTACGCGGGAAGATGCCGTCGACGGTTGAGATCGAAGAGTTCTTCTC 318

QY 518 GGAGCTAGAGATCCAGACGATAACGAAGCAATTCATAAGTACAACTTCGATAT 577

Db 317 CCGACGGGAAA-----AGTACCAGCAACAGCGGATTCGAGAGAAGTACAATACGATAT 264

QY 578 TGTCATGACCAACCGCTTGAAGTTCGCTTACAAGTGGGATCG 619

Db 263 CGTGAAGATGCCCCCATCGAGGGCGGTACCAAGTGGGTTCG 222

## RESULT 13

CO408372

## LOCUS

VRK51277 Vitis riparia bud - VRK Vitis riparia cDNA clone VRK51.2

5', mRNA sequence.

## DEFINITION

CO408372

## ACCESSION

CO408372

## VERSION

EST.

## KEYWORDS

Vitis riparia

## SOURCE

Vitis riparia

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Vitaceae; Vitis.

## REFERENCE

1 (bases 1 to 747)

## AUTHORS

Fennell, A. and Mathiason, K.

## TITLE

Expressed sequence tags from Vitis riparia buds

## JOURNAL

Unpublished (2004)

## COMMENT

Contact: Anne Fennell  
Horticulture, Forestry, Landscape and Parks Department  
South Dakota State University  
Northern Plains Biostress Laboratory, Box 2140A, Brookings, SD  
57007-0996, USA

Tel: 605 688 6373

Fax: 605 688 4713

Email: Anne.Fennell@sdstate.edu

Seq primer: T7.

## FEATURES

source

Location/Qualifiers  
1..747

/organism="Vitis riparia"

/mol\_type="mRNA"

/db\_xref="taxon:96939"

/clone="VRK512"

/dev\_stage="paradormant"

/lab\_host="DH10B"

/clone\_lib="Vitis riparia bud - VRK"

/note="Organ: bud; Vector: pSport 1; Site 1: SalI; Site 2: NotI; VRK is a cDNA library of Vitis riparia paradormant buds. Compound paradormant buds were collected from actively growing shoots on insect and disease free vines. The directionally oriented library was constructed according to Gibco BRL Superscript Plasmid System for cDNA synthesis and plasmid cloning."

## ORIGIN

Query Match 11.2%; Score 70.4; DB 7; Length 747;

Best Local Similarity 58.9%; Pred. No. 3.1e-09;

Matches 166; Conservative 0; Mismatches 101; Indels 15; Gaps 2;

QY 347 CGAAACCGAAACCTCAACATTCATCCAGCAATTTGAGAAAGAGACGAGTCAGTCGAG 406

Db 340 CGAAACTGANAACCTCAAGTATAGCGAGCGGAGGTTTCAGTAGAGACCACTCCAGTCGAG 399

QY 407 TGAG-----GGTTGGGAGAAACGACAAAGAAATGGAATCATCATCGGCAACGAA 457

Db 400 CGAGCTCCACGCTGATTTCAGCTGAGATGGAGTCTACGGGAGAGACTACAGCGGCCAAACC 459

QY 458 GAGAAAACACCGCGGGGTGAGAAAGACTCCAAAGCGCGGGGAGATTGAGATTGTTCTC 517

Db 460 GCGGCGGAAATCTACGCGGGAAGATGCCGTCGACGGTTGAGATCGAAGAGTTCTTCTC 519

QY 518 GGAGCTAGAGATCCAGACGATAAGAGAACCAATTCATAGAAAAGTACAACCTTCGATAT 577

Db 520 CCGAGCGGAAA-----AGTACCAGCAACAGCGGATTCGAGAGAAGTACAACCTACGATAT 573

QY 578 TGTCATGACCAACCGCTTGAAGTTCGCTTACAAGTGGGATCG 619

Db 574 CGTGAAGATGCCCCCATCGAGGGCGGTACCAAGTGGGTTCG 615

## RESULT 14

CV234322/c

## LOCUS

WS01214.B21\_H23

PT-GT-FL-A-3

Populus balsamifera subsp. trichocarpa

CDNA clone WS01214\_H23 3', mRNA sequence.

CV234322

CV234322.1

GI:52391767

EST.

Populus balsamifera subsp. trichocarpa (Populus trichocarpa)

Populus balsamifera subsp. trichocarpa

Eukaryota; Viridiplantae; Streptophyta

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; euroids I; Malpighiales; Salicaceae; Populus.

1 (bases 1 to 712)

Ralph, S., Cooper, D., Kolosova, N., Oddy, C., Butterfield, Y.,

Kirkpatrick, R., Liu, J., Palmquist, D., Scott, J., Barber, S., Yang, G.,

Babakaiff, R., Brown-John, M., Chand, S., Featherstone, R., Masson, A.,

Mayo, M., Moran, J., Olson, T., Wong, D., Ritland, C.E., Siddiqui, A.,

CV234322 712 bp mRNA linear EST 21-SEP-2004  
WS01214.B21\_H23 PT-GT-FL-A-3 Populus balsamifera subsp. trichocarpa  
CDNA clone WS01214\_H23 3', mRNA sequence.

CV234322

CV234322.1

GI:52391767

EST.

Populus balsamifera subsp. trichocarpa (Populus trichocarpa)

Populus balsamifera subsp. trichocarpa

Eukaryota; Viridiplantae; Streptophyta

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; euroids I; Malpighiales; Salicaceae; Populus.

1 (bases 1 to 712)

Ralph, S., Cooper, D., Kolosova, N., Oddy, C., Butterfield, Y.,

Kirkpatrick, R., Liu, J., Palmquist, D., Scott, J., Barber, S., Yang, G.,

Babakaiff, R., Brown-John, M., Chand, S., Featherstone, R., Masson, A.,

Mayo, M., Moran, J., Olson, T., Wong, D., Ritland, C.E., Siddiqui, A.,



Holt,R., Jones,S., Marra,M., Ellis,B.E., Douglas,C., Ritland,K. and Bohlmann,J.  
The poplar transcriptome: Analysis of expressed sequence tags from multiple cDNA libraries  
Unpublished (2004)  
Contact: Joerg Bohlmann  
Genome BC forest genomics program  
University of British Columbia  
UBC Biotechnology Laboratory, 6174 University Boulevard, Rm. 237, Vancouver, British Columbia, Canada, V6T 1Z3  
Tel: 1-604-822-0282  
Fax: 1-604-822-6097  
Email: bohlmann@interchange.ubc.ca  
Plate: WS01214 row: H column: 23  
High quality sequence stop: 712  
POLYA=Yes.

# FEATURES

Location/Qualifiers  
1. 712  
/organism="Populus balsamifera subsp. trichocarpa"  
/mol\_type="mRNA"  
/cultivar="383-2499 (Nisqually-1)"  
/sub\_species="trichocarpa"  
/db\_xref="taxon:3694"  
/clone="WS01214\_H23"  
/sex="Female"  
/lab\_host="E. coli DH10B T1 phage resistant cells"  
/clone\_lib="PT-GT-FL-A-3"  
/notes="Vector: pBluescript II SK (+) XR; Site 1: SstI (5' end of cDNA); Site 2: XhoI (3' end of cDNA); Young and mature leaves, along with green stems, from 8 year old trees harvested within the Boise Cascade region of Washington state on May 15th, 2001. mRNA was isolated from each tissue source independently and equal quantities of mRNA from each tissue were then pooled. cDNA was prepared from 20 micrograms of mRNA according to the full-length cDNA library construction method described by Carninci P. et al. (2000), Genome Research 10(10):1617-1630 and directionally ligated into the pBluescript II SK (+) XR vector digested with SstI (5' end) and XhoI (3'). Plasmid DNA was then transformed by electroporation into DH10B cells (Invitrogen) for propagation."

# ORIGIN

Query Match 11.2%; Score 70; DB 7; Length 712;  
Best Local Similarity 57.7%; Pred. No. 4.1e-09;  
Matches 209; Conservative 0; Mismatches 135; Indels 18; Gaps 4;  
QY 261 TCCTGCTGTTCCAGCAGTGAATCGAAGAAATCGCGAAGACAGTTCGTCGTTGGTGA 320  
DB 570 TCCTGCTGTTCCAGCAGTGAATCGAAGAAATCGCGAAGACAGTTCGTCGTTGGTGA 514  
QY 321 GATCTGGAGGATCATCAATCGAAGAAATCGCGAAGACAGTTCGTCGTTGGTGA 380  
DB 513 GATCTGGAGGATCATCAATCGAAGAAATCGCGAAGACAGTTCGTCGTTGGTGA 460  
QY 381 TTCAGAAAAGAGACGAGTCCAGTGAAGAGGTTTCGGAG- - -AAACGACACAGAAATG 437  
DB 459 TTCAGTGAAGAAACCACTCTTCAACGAGTTTTCAGCGATGTACTCGCGGAGCGGTG 400  
QY 438 GAATCATATCGCAACGAGAGAAACACCGGGGGTGAAGAGACTCAACCGCGGG 497  
DB 399 GAGAAGAAAGAGAAATCTCACAGGAGAAATGACCGGCTGTGAAATGCGGATCAGGCT 340  
QY 498 GAGATTGAGGATTTGTTCTCGGAGTGAAGTCCAGAGTCCAGAGTAAAGAAAGCAATTCATA 557  
DB 339 GAGATCGATCGTTTTCGGGGGGCAGAGAG- - -GAGGACGAGAAAGATTGCA 286  
QY 558 GAAAGTACAACTTCGATATGTCAATGACGAAACCGCTTGAAGGTCGCTACAGTGGAT 617  
DB 285 GAGAAGTACAACTTACGATGTGTGAAGGATTTTCCAGTGGAGGTCGCTACCAAGTGGAT 226  
QY 618 CG 619

Db 225 TG 224  
RESULT 15  
CV242992/c  
LOCUS  
DEFINITION  
CV242992.1 GI:52495967  
EST.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
The poplar transcriptome: Analysis of expressed sequence tags from multiple cDNA libraries  
Unpublished (2004)  
Contact: Joerg Bohlmann  
Genome BC forest genomics program  
University of British Columbia  
UBC Biotechnology Laboratory, 6174 University Boulevard, Rm. 237, Vancouver, British Columbia, Canada, V6T 1Z3  
Tel: 1-604-822-0282  
Fax: 1-604-822-6097  
Email: bohlmann@interchange.ubc.ca  
Plate: WS02516 row: J column: 17  
High quality sequence stop: 919  
POLYA=Yes.  
Location/Qualifiers  
1. 919  
/organism="Populus balsamifera subsp. trichocarpa"  
/mol\_type="mRNA"  
/cultivar="Wild clone"  
/sub\_species="trichocarpa"  
/db\_xref="taxon:3694"  
/clone="WS02516\_J17"  
/sex="Male"  
/lab\_host="E. coli DH10B T1 phage resistant cells"  
/clone\_lib="PT-MB-N-A-15"  
/notes="Vector: pBluescript II SK (+) XR; Site 1: EcoRI (5' end of cDNA); Site 2: XhoI (3' end of cDNA); Terminal vegetative buds from 20 year old trees harvested near Corvallis, Oregon on September 19th, 2001. cDNA was prepared from 5 micrograms of mRNA and directionally ligated into the pBluescript II SK (+) XR vector using the pBluescript II XR cDNA Library Construction Kit according to manufacturer's instructions with modifications (Stratagene). Plasmid DNA was then transformed by electroporation into DH10B cells (Invitrogen) for propagation. Normalization was applied according to published methods [Bonaldo M.P. et al. (1996) Genome Research 6(9):791] in order to reduce the abundance of highly expressed transcripts."

# ORIGIN

Query Match 11.2%; Score 70; DB 7; Length 919;  
Best Local Similarity 57.7%; Pred. No. 4.3e-09;  
Matches 209; Conservative 0; Mismatches 135; Indels 18; Gaps 4;  
QY 261 TCCTGCTGTTCCAGCAGTGAATCGAAGAAATCGCGAAGACAGTTCGTCGTTGGTGA 320  
DB 666 TCCTGCTGTTCCAGCAGTGAATCGAAGAAATCGCGAAGACAGTTCGTCGTTGGTGA 610  
QY 321 GATCTGGAGGATCATCAATCGAAGAAATCGCGAAGACAGTTCGTCGTTGGTGA 380

609	GATCTGGAGG-----CGAAGAGTTCCGAACCGAAAGCTCAGCTGCAATCACAGGAAA	556						
381	TTCAGAAAAGAGACGAGTCCAGTGAGTGAAGGTCTTTGGGAG---AAACGACAACAGAAATG	437						
555	TTCAGTAGAGACACACTCTCTTCAGCGAGTTTCACGGATGTACTCGCGGCAGCCGTG	496						
438	GAATCATCATCGGCNACGAAGAAAAACAACCGGGGTGAGGAAGACTCCAACGCCGGCG	497						
495	GAGAAGAAAGAAATTCTCACAGGAGAAAGTCACCGGCTGTCAAATGCCGAGTCAGGCT	436						
498	GAGATTGAGGATTTGTTCTCGGAGCTAGAGATCCAGACGATAAGAAGACCAATTGATA	557						
435	GAGATCGATGCGTTTTTCGCGGGGCAGAGAG-----GAGGAGCAGAAAAAGATTTGCA	382						
558	GAAGAAGTCAAACTTCGATATTGTCAATACGAAACCGCTTGTAAGGTTCGCTACAAGTGGGAT	617						
381	GAGAAGTACAACACTAGATGTTGTGAAGGATTTGCCAGTGGAGGTCGCTACCAGTGGATT	322						
618	CG 619							
321	TG 320							
D <sub>b</sub>								

Search completed: September 30, 2005, 11:32:37  
Job time : 2876 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 30, 2005, 11:35:38 ; Search time 4142 Seconds  
(without alignments)  
2444.988 Million cell updates/sec

Title: US-09-980-758A-8  
Perfect score: 1045  
Sequence: 1 FRDLPNPREKXMSERREL.....NFDVNDPELEGRYKWDRLX 209

Scoring table:

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Ygapext 0.5			
Fgapop 6.0			
Fgapext 7.0			
Delop 6.0			
Delext 7.0			

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-O=/cn2 1/USPTO.spool/US9980758/runat.30092005.100632.510/app.query.fasta\_1.391  
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOPCLO=0 -LOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45  
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Database :

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1: gb.ba.\*

2: gb.htg.\*

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4: gb.om.\*

5: gb.ov.\*

6: gb.pat.\*

7: gb.ph.\*

8: gb.pl.\*

9: gb.pr.\*

10: gb.ro.\*

11: gb.ste.\*

12: gb.sy.\*

13: gb.un.\*

14: gb.vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1037	99.2	626	6	BD267733 Method of
2	1007	96.4	824	6	AX008797 Sequence
3	1007	96.4	824	6	AX463066 Sequence
4	1007	96.4	840	8	AF106705 Arabidops

#### ALIGNMENTS

RESULT 1	BD267733	BD267733.1	GI:33077501
LOCUS	BD267733	Method of promoting plant cell proliferation by functionally inhibiting plant cyclin inhibitor gene.	626 bp DNA linear PAT 17-JUL-2003
DEFINITION	BD267733	Method of promoting plant cell proliferation by functionally inhibiting plant cyclin inhibitor gene.	
ACCESSION	BD267733	BD267733.1	GI:33077501
VERSION	JP 2002543823-A/4.	JP 2002543823-A/4.	
KEYWORDS	Arabidopsis thaliana (thale cress)	Arabidopsis thaliana (thale cress)	
SOURCE	Arabidopsis thaliana	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	
ORGANISM	Arabidopsis thaliana	1 (bases 1 to 626)	
REFERENCE	1	Roberts, J. and Kelly, B.	
AUTHORS	Roberts, J. and Kelly, B.	Method of promoting plant cell proliferation by functionally inhibiting plant cyclin inhibitor gene	
TITLE	Method of promoting plant cell proliferation by functionally inhibiting plant cyclin inhibitor gene	Patent: JP 2002543823-A 4 24-DEC-2002;	
JOURNAL	PATENT: JP 2002543823-A 4 24-DEC-2002;	FRED HUTCHINSON CANCER RESEARCH CENTER	
COMMENT	OS Arabidopsis thaliana (thale cress)	PN JP 2002543823-A/4	
	PD 24-DEC-2002	PP 15-MAY-2000	JP 2000618299
	PR 14-MAY-1999	US 60/134373	
	PI JAMES ROBERTS, BETH KELLY		
	PC A01H5/00, C12N5/10, C12N15/09, C12N15/00, C12N5/00	CC	Method of
	Promoting plant cell proliferation by functionally	CC	
	inhibiting		

AJ301557 Arabidops  
AP000419 Arabidops  
AX008798 Sequence  
AX463067 Sequence  
AJ301558 Arabidops  
AF208692 Arabidops  
AC011807 Arabidops  
AB029483 Pisum sat  
AY085749 Arabidops  
AX008791 Sequence  
AX463060 Sequence  
AY439104 Glycine m  
AJ517189 Nicotiana  
U94772 Arabidopsis  
CQ803686 Sequence  
BD267732 Method of  
AJ251851 Arabidops  
AX463077 Sequence  
AY088290 Arabidops  
A98054 Sequence 1  
AR490032 Sequence  
BD075687 Cyclin-de  
AK176528 Arabidops  
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AX008793 Sequence  
AX463062 Sequence  
AJ301555 Arabidops  
AY439101 Glycine m  
AK176575 Arabidops  
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AX008805 Sequence  
AX463073 Sequence  
AJ002173 Chenopodi  
AK117586 Arabidops  
AJ441250 Lycopersi  
CQ803830 Sequence  
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CC plant cyclin inhibitor gene  
FH Key Location/Qualifiers  
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Pred. No.: 1.69e-77 Length: 626  
Score: 1037.00 Matches: 207  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.23% Indels: 0  
DB: 6 Gaps: 0

US-09-980-758A-8 (1-209) x BD267733 (1-626)

QY 2 ArgAspLeuProLysAsnProArgGluLysLysMetSerGluArgLysArgGluLeuAla 21  
Db 3 CGAGATTACCCAAATAATCCAGAGAGAAAAAATGACGAGAGAAACGAGAGCTTCCA 62  
QY 22 GluGluAlaSerSerThrSerPheSerProLeuLysLysThrLysLeuAsnAspSerSer 41  
Db 63 GNAGAGGCTTCNAGCACAGCTTCTCACCACTGAGAGAAACGAAGCTTAATGATTTCTCT 122  
QY 42 AspSerSerProAspSerHisAspValIleValPheAlaValSerSerSerValAla 61  
Db 123 GATTTCATCACCGGACTCTCATGACGTCTCGTCTCCGGGTTTCATCTTCTCCGTTGCT 182  
QY 62 SerSerAlaAlaLeuAlaSerAspGluCysSerValThrIleGlyGluGluSerAsp 81  
Db 183 TCGTCGGCGGCTTTAGCTGTGATGAATGTTCCGTTACCATCGGTGGAGAGAAAGTGAT 242  
QY 82 GlnSerSerSerIleSerSerGlyCysPheThrSerGluSerLysGluIleAlaLysAsn 101  
Db 243 CAGTCTCTCGAGTATCAGCTCCGGTGTGTTTCACCACTGATCGAAGAATTCGCGNAGAAC 302  
QY 102 SerSerSerPheGlyValAspLeuGluAspHisGlnIleGluThrGluThrSer 121  
Db 303 AGTTCGTCGTTGTTGTTAGATCTGAGGATCATCAATCGAAACCGAAACCGAAACCTCA 362  
QY 122 ThrPheIleThrSerAsnPheArgLysGluThrSerProValSerGluGlyLeuGlyGlu 141  
Db 363 ACATTATCACCCAGCAATTTAGAAAGAGAGACGAGTCCAGTGAGTGGGGTTTGGGAGAA 422  
QY 142 ThrThrThrGluMetGluSerSerSerAlaThrLysArgLysGlnProGlyValArgLys 161  
Db 423 ACGACAAACAGAAATGGAATCATATCGACACGAGAGAGAAACAACCCGGGGTGGGAG 482  
QY 162 ThrProThrAlaAlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAspLys 181  
Db 483 ACTCAACCGCGCGGAGATTGAGGATTGTTCTCGGAGCTAGAGAGTCCAGACGATAAG 542  
QY 182 LysLysGlnPheIleGluLysTyrsAsnPheAspIleValAsnAspGluProLeuGluGly 201  
Db 543 AAGAAGCAATTCATAGAAAGTACAACTTCGATATTGTCAATGACGAACCCGCTTGAAGGT 602  
QY 202 ArgTyLysTrpAspArgLeu 208  
Db 603 CGCTACAGTGGGATCGACTT 623

RESULT 2  
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LOCUS AX008797 824 bp DNA linear PAT 06-SEP-2000  
DEFINITION Sequence 7 from Patent WO9964599.  
ACCESSION AX008797  
VERSION AX008797.1 GI:9996261  
KEYWORDS

SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi  
REFERENCE  
AUTHORS Fowke,L.C., Wang,H. and Crosby,W.L.  
TITLE Cyclin-dependent kinase inhibitors as plant growth regulators  
JOURNAL Patent: WO 9964599-A 7 16-DEC-1999;  
FOWKE LARRY C (CA); WANG HONG (CA); AGRICULTURE AND AGRIFOOD CANAD  
(CA); CANADA NAT RES COUNCIL (CA); CROSBY WILLIAM L (CA); UNIV  
SASKATCHEWAN TECHNOLOGIES (CA)  
FEATURES  
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Location/Qualifiers  
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Pred. No.: 7.53e-75 Length: 824  
Score: 1007.00 Matches: 202  
Percent Similarity: 99.51% Conservative: 0  
Best Local Similarity: 99.51% Mismatches: 1  
Query Match: 96.36% Indels: 0  
DB: 6 Gaps: 0

US-09-980-758A-8 (1-209) x AX008797 (1-824)

QY 6 LysAsnProArgGluLysLysMetSerGluArgLysArgGluLeuAlaGluGluAlaSer 25  
Db 28 AAAAATCCAGAGAGAAAAAATGACGAGAGAAAGCGAGAGCTTGCAGAGAAAGCTTCA 87  
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Db 88 AGCACAGCTTCTCACCACCTGAGAAACGAGCTTAATGATTTCTTGATTCATCACCG 147  
QY 46 AspSerHisAspValIleValPheAlaValSerSerSerSerValAlaSerSerAlaAla 65  
Db 148 GACTCTCATGACGTCATCGTCTTCGCGTTTCATCTTCTTCGTTGCTTCGTCGCGCT 207  
QY 66 LeuAlaSerAspGluCysSerValThrIleGlyGluGluSerAspGluSerSerSer 85  
Db 208 TTAGCGCTGTGATGATGTTCCGTTACCATCGGTGGAGAAAGTGATCAGTCTCGAGT 267  
QY 86 IleSerSerGlyCysPheThrSerGluSerLysGluIleAlaLysAsnSerSerPhe 105  
Db 268 ATCAGTCCCGTTGTTTCCACCGATTCGAAAGAAATCGCGAAGAACAGTTCGTCGTTT 327  
QY 106 GlyValAspLeuGluAspHisGlnIleGluThrGluThrGluThrSerThrPheIleThr 125  
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QY 126 SerAsnPheArgLysGluThrSerProValSerGluGlyLeuGlyGluThrThrGlu 145  
Db 388 AGCAATTTCAAAAAGAGACGAGTCCAGTCCAGTGGGGTTTGGGAGAAACACACAGAA 447  
QY 146 MetGluSerSerAlaThrLysArgLysGlnProGlyValArgLysThrProThrAla 165  
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QY 166 AlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAspLysLysLysGlnPhe 185  
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QY 186 IleGluLysTyrsAsnPheAspIleValAsnAspGluProLeuGluGlyArgTyLysTrp 205  
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QY 206 AspArgLeu 208  
Db 628 GATCGACTT 636

Db 568 ATGAAAGTACAACTTCGATATTGTCAATGACGACCGCTTGAAAGTCGCTCAAGTGG 627  
 Qy 206 AspArgLeu 208  
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 Db 628 GATCGACTT 636

RESULT 4  
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 LOCUS Arabidopsis thaliana cyclin dependent kinase inhibitor (ACK1) mRNA, complete cds.  
 ACCESSION AF106705  
 VERSION AF106705.2  
 KEYWORDS GI:8789104  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

REFERENCE 1 (bases 1 to 840)  
 AUTHORS Park, S.C. and Cho, J.W.  
 TITLE A novel cyclin dependent kinase inhibitor (ack1)  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 379 to 789)  
 AUTHORS Park, S.C. and Cho, J.W.  
 TITLE Direct Submission  
 JOURNAL Submitted (14-NOV-1998) Kumho Life & Environmental Science Laboratory, 572 Sangamdong Kwangsanku, Kwangju 506-712, South Korea

REFERENCE 3 (bases 1 to 840)  
 AUTHORS Park, S.C. and Cho, J.W.  
 TITLE Direct Submission  
 JOURNAL Submitted (28-JUN-2000) Kumho Life & Environmental Science Laboratory, 572 Sangamdong Kwangsanku, Kwangju 506-712, South Korea

REMARK Sequence update by submitter  
 COMMENT On Jun 28, 2000 this sequence version replaced gi:8574522.

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ORIGIN  
 Alignment Scores:  
 Pred. No.: 7,72e-75 Length: 840  
 Score: 1007.00 Matches: 202  
 Percent Similarity: 99.51% Conservative: 0  
 Best Local Similarity: 99.51% Mismatches: 1  
 Query Match: 96.36% Indels: 0  
 DB: 8 Gaps: 0

US-09-980-758A-8 (1-209) x AF106705 (1-840)

Qy 6 LysAsnProArgGluLysLysMetSerGluArgGluLeuAlaGluGluAlaSer 25  
 Db 2 AAAAATCCAGAGAGAAAAAATGAGCGAGAGAAAGCGAGAGCTTCGAGAAGAAGCTTCA 61  
 Qy 26 SerThrSerPheSerProLeuLysLysThrLysLeuAsnAspSerSerAspSerPro 45  
 Db 62 AGCACAAAGCTTCTCACCACTGAAGAAACGAAAGCTTAATGATTTCTTCTGATTCATCACCG 121  
 Qy 46 AspSerHisAspValIleValPheAlaValSerSerSerValAlaSerSerAlaAla 65

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Db 122 GACTCTCATGAGTTCATCGTCTTCGCGGTTCATCTCTCGTTGCTTCGTCGCGGCT 181  
Qy 66 LeuAlaSerAspGluCySerValThrIleGlyGlyGluGluSerAspGlnSerSerSer 85  
Db 182 TTAGCGTCTGATGAATGTTCCGTTACCATCGGTGAGAGAAAGTATCAGTCTCTCGAGT 241  
Qy 86 IleSerSerGlyCySerPheThrSerGluSerLysGluIleAlaLysAsnSerSerSerPhe 105  
Db 242 ATCAGCTCCGGTTGTTTCCACAGTGAATCGAAAGAAATCGGAGAAACAGTTCGTCGTTT 301  
Qy 106 GlyValAspLeuGluAspHisGlnIleGluThrGluThrGluThrSerThrPheIleThr 125  
Db 302 GGTGTAGATCTGGAGGATCATCAATCGAACCGAAACCGAAACCTCAACATTTCATCACC 361  
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Db 602 GATCGACTT 610

RESULT 5  
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DEFINITION (krp6 gene).  
ACCESSION AJ301557  
VERSION 1.1 GI:14422294  
KEYWORDS cyclin-dependent kinase inhibitor; krp6 gene.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1  
De Veylder, L., Beeckman, T., Beeckman, T., Krols, L., Terras, F.,  
Landrieu, I., van der Schueren, E., Maes, S., Naudts, M. and Inze, D.  
Functional analysis of cyclin-dependent kinase inhibitors of

Arabidopsis  
JOURNAL Plant Cell 13 (7), 1653-1668 (2001)  
MEDLINE 21342510  
PUBMED 11449057  
REFERENCE 2 (bases 1 to 591)  
de Veylder, L.  
Direct Submission  
TITLE Submitted (31-OCT-2000) De Veylder L., Departement Plantegenetica,  
Vlaams Interuniversitair Instituut voor Biologie (VIB), K.L.  
JOURNAL Ledeganckstraat 35, B-9000 Gent, BELGIUM

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ORIGIN

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Best Local Similarity: 99.49% Mismatches: 1  
Query Match: 92.73% Indels: 0  
DB: Gaps: 0

US-09-980-758A-8 (1-209) x ATH301557 (1-591)  
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Qy 33 LysLysThrLysLeuAsnAspSerSerAspSerSerProAspSerHisAspValIleVal 52  
Db 61 AAGAAACGAAGCTTAATGATCTTTCGATTCATACCGGACTCTCATGAGTCATCGTC 120  
Qy 53 PheAlaValSerSerSerValAlaSerSerAlaAlaLeuAlaSerAspGluCySer 72  
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Db 541 ATTGCTAATGCAACCGCTTGAAGGTCGCTACAAAGTGGGATCGACTT 588

RESULT 6  
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LOCUS AP000419 81875 bp DNA linear PLN 14-FEB-2004  
DEFINITION Arabidopsis thaliana genomic DNA, chromosome 3, Pl clone: MW11.  
ACCESSION AP000419 BA000014  
VERSION AP000419.1 GI:5832740  
KEYWORDS Arabidopsis thaliana (thale cress)  
SOURCE Arabidopsis thaliana  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

AUTHORS Kaneko,T., Katoh,T., Sato,S., Nakamura,A., Asamizu,E. and Tabata,S.  
 TITLE Structural analysis of Arabidopsis thaliana chromosome 3. II.  
 JOURNAL Sequence features of the 4,251,695 bp regions covered by 90 P1, TAC  
 MEDLINE DNA Res. 7 (3), 217-221 (2000)  
 PUBMED 20363099  
 10907853  
 2 (bases 1 to 81875)  
 REFERENCE Kaneko,T., Katoh,T., Sato,S., Nakamura,Y., Asamizu,E. and Tabata,S.  
 AUTHORS Direct Submission  
 TITLE Submitted (03-SEP-1999) Yasukazu Nakamura, Kazusa DNA Research  
 JOURNAL Institute, Department of Plant Gene Research; 1532-3, Yana,  
 Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp,  
 Tel:81-438-52-3935, Fax:81-438-52-3934)  
 COMMENT Address for correspondence: kaos@kazusa.or.jp  
 For the latest information on annotation of this clone, please see  
 http://www.kazusa.or.jp/kaos/cgi-bin/agd/graph.cgi?c=Mv111  
 Genes with similarity to proteins in the databases are described in  
 'product' or 'note' qualifiers. Genes that have no significant  
 protein similarity are described as 'unknown protein'.  
 The software programs used to predict genes include: Grail  
 (Informatics Group, Oak Ridge National Laboratory,  
 http://compbio.ornl.gov/Grail-1.3/),  
 GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),  
 NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of  
 Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and  
 SplicePredictor (Volker Brendel, Stanford University,  
 http://grm1.nli.zool.iastate.edu/cgi-bin/sp.cgi).  
 Genes encoding tRNAs are predicted by tRNAscan-SE  
 (Sean Eddy, Washington University School of Medicine, St. Louis,  
 http://genome.wustl.edu/eddy/tRNAscan-SE/).  
 This sequence may not be the entire insert of this clone. It may be  
 shorter because we remove overlaps between neighboring submissions.  
 The 5' clone is MHP21 and the 3' clone is MUD14.

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CDS

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US-09-980-758A-8 (1-209) x AF000419 (1-81875)

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REFERENCE						
AUTHORS	Fowke,L.C., Wang,H. and Crosby,W.L.					
TITLE	Cyclin-dependent kinase inhibitors as plant growth regulators					
JOURNAL	Patent: WO 9964599-A 8 16-DEC-1999;					
	FOWKE LARRY C (CA); WANG HONG (CA); AGRICULTURE AND AGRIFOOD CANAD					
	(CA); CANADA NAT RSC COUNCIL (CA); CROSBY WILLIAM L (CA); UNIV					
	SASKATCHEWAN TECHNOLOGIES (CA)					



**REFERENCE**  
**AUTHORS** Powke,L.C., Wang,H. and Zhou,Y.  
**TITLE** Modulation of plant cyclin-dependent kinase inhibitor activity  
**JOURNAL** Patent: WO 0250292-A 8 27-JUN-2002;  
University of Saskatchewan Technologies (CA); Minister of Agriculture and Agrifood Canada (CA)

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Qy    177  SerProAspAspLysLysGlnPheIleGluLysTyrsenPheAspIleValAsnAsp 196
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RESULT 9  
ATH301558  
LOCUS  
DEFINITION Arabidopsis thaliana mRNA for cyclin-dependent kinase inhibitor 7 (krp7 gene).  
ACCESSION AJ301558  
PLN 26-JUL-2000



Pred. No.:	5.09e-17	Length:	4116	
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Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	30.91%	Indels:	0	
DB:	8	Gaps:	0	
US-09-980-758A-8 (1-209) X F208692 (1-4116)				
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QY	26	SerThrSerPheSerProLeuLysLysThrLysLeuAsnAspSerSerAspSerPro 45		
Db	3975	AGCACAAAGTCTCCACCACCTGAAGAAACGAAGCTTAATGATTCTTCGATTCATCACCG 4034		
QY	46	AspSerHisAspValIleValPheAlaValSerSerSerValAlaSerSerAlaAla 65		
Db	4035	GACTCTCATGACGTATCGTTCGCGGTTTCATCTTCGCTTCGTCGCGGCT 4094		
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RESULT 11				
AC011807				
LOCUS	AC011807	104679 bp	DNA	linear PLN 13-SEP-2000
DEFINITION	Arabidopsis thaliana chromosome I BAC F14J22 genomic sequence,			
complete sequence.				
AC011807				
AC011807.4	GI:6693374			
HTG.				
Arabidopsis thaliana (thale cress)				
Arabidopsis thaliana				
Eukaryota: Viridiplantae; Streptophyta: Embryophyta: Tracheophyta;				
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;				
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.				
1 (bases 1 to 104679)				
REFERENCE				
AUTHORS	Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F.,			
Altafi,H., Araujo,R., Huizar,L., Rowley,D., Buehler,E., Dunn,P.,				
Gonzalez,A., Kremenetskaia,I., Kim,C., Lenz,C., Li,J., Liu,S.,				
Luros,S., Schwartz,J., Shinn,P., Toriumi,M., Vysotskaia,V.S.,				
Walker,M., Yu.G., Ecker,J., Theologis,A. and Davis,R.W.				
Unpublished				
2 (bases 1 to 104679)				
REFERENCE				
AUTHORS	Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F.,			
Altafi,H., Nguyen,M., Lam,B., Southwick,A., Bel,Q., Buehler,E.,				
Chin,C., Chlou,J., Choi,E., Dunn,P., Gonzalez,A., Howng,B., Kim,C.,				
Koo,T., Lee,J.M., Lenz,C., Li,J., Liu,A., Liu,K., Liu,S.,				
Mukharasy,N., Pham,P., Sakano,H., Schwartz,J., Shinn,P.,				
Thaveri,A., Toriumi,M., Vaysberg,M., Walker,M., Yu.G., Ecker,J.,				
Theologis,A. and Davis,R.W.				
Direct Submission				
TITLE	Submitted (15-OCT-1999) DNA Sequencing and Technology Center,			
JOURNAL	Stanford University, 855 California Avenue, Palo Alto, CA 94304,			
USA				
3 (bases 1 to 104679)				
REFERENCE				
AUTHORS	Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F.,			
Altafi,H., Araujo,R., Huizar,L., Rowley,D., Buehler,E., Dunn,P.,				
Gonzalez,A., Kremenetskaia,I., Kim,C., Lenz,C., Li,J., Liu,S.,				
Luros,S., Schwartz,J., Shinn,P., Toriumi,M., Vysotskaia,V.,				
Walker,M., Yu.G., Ecker,J., Theologis,A. and Davis,R.W.				
Direct Submission				
TITLE	Submitted (14-JAN-2000) DNA Sequencing and Technology Center,			
JOURNAL	Stanford University, 855 California Avenue, Palo Alto, CA 94304,			
USA				
4 (bases 1 to 104679)				
REFERENCE				
AUTHORS	Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F.,			
Altafi,H., Nguyen,M., Lam,B., Southwick,A., Ecker,J., Theologis,A.				
and Davis,R.W.				
Direct Submission				
TITLE	Submitted (13-SEP-2000) DNA Sequencing and Technology Center,			
JOURNAL				

Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA

On Jan 14, 2000 this sequence version replaced gi:6692246. Bases 92948-104679 of IGF clone F14J22 overlap with bases 1-11732 of IGF clone F13F21 (gb|AC007504).

e-mail for correspondence: arab@sequence.stanford.edu  
Genes with similarity to proteins in the databases are named 'putative', '-like' or 'similar to'. Genes that have EST similarity but no significant protein similarity are described as 'unknown proteins'. Genes that are annotated based only on gene prediction software are described as 'hypothetical proteins'. The gene prediction programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/section/index.html), GENSCAN (Chris Burge, http://genes.mit.edu/GENSCAN.), FEXA (Victor Solovyev, http://genomic.sanger.ac.uk/gf/gf.shtm), and NetPlantGene (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/NetPlantGene.html).

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	EKVFTNVYKNLSDEELNKVFGFVGTTCVIMRDGSGKSGFGVFNFENSD
	AARAVDALNGKTFDDKFWVGAKQKSERETELKQKFEQSLKEAADKSGSNLYKNL



Qy	78	GlUGluserAspGlnSerSerSerGlyCysPheThrSerGluSerLysGlu	97
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Qy	197	GlUGluserGluGlyArgTyLysTrpAspArgLeu	208
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RESULT 13

AY085749

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

780 bp mRNA linear PLN 14-APR-2000

Arabidopsis thaliana clone 17682 mRNA, complete sequence.

AY085749.1 GI:21404459

FLI CDNA.

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 780)

Haas,B.J., Volfovsky,N., Town,C.D., Troughan,M., Alexandrov,N., Feldmann,K.A., Flavell,R.B., White,O. and Salzberg,S.L.

Full-length messenger RNA sequences greatly improve genome annotation

Genome Biol. 3 (6), RESEARCH0029 (2002)

22088475

12093376

2 (bases 1 to 780)

Brover,V., Troughan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and Feldmann,K.

Full-length cDNA from Arabidopsis thaliana

Unpublished

3 (bases 1 to 780)

Brover,V., Troughan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and Feldmann,K.

Direct Submission

Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA

This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the Ws or Llaer ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0.

Genset carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.

FEATURES  
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## ORIGIN

Alignment Scores:  
Pred. No.: 3 96a-06 Length: 780  
Score: 181.00 Matches: 63  
Percent Similarity: 42.24% Conservative: 35  
Best Local Similarity: 27.16% Mismatches: 68  
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US-09-980-758A-8 (1-209) x AY085749 (1-780)

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## RESULT 14

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DEFINITION Sequence 1 from Patent WO9964599.  
ACCESSION AX008791  
VERSION AX008791.1 GI:9996255

## KEYWORDS

SOURCE Arabidopsis thaliana (thale cress)

## ORGANISM

Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

## REFERENCE

1 Fowke,L.C., Wang,H. and Crosby,W.L.

Cyclin-dependent kinase inhibitors as plant growth regulators

Patent: WO 9964599-A 1 16-DEC-1999;

FOWKE LARRY C (CA); WANG HONG (CA); AGRICULTURE AND AGRIFOOD CANAD

(CA); CANADA NAT RES COUNCIL (CA); CROSBY WILLIAM L (CA); UNIV

SASKATCHEWAN TECHNOLOGIES (CA)

## FEATURES

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## ORIGIN

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Best Local Similarity: 27.16% Mismatches: 68  
Query Match: 17.32% Indels: 66  
DB: 6 Gaps: 10

US-09-980-758A-8 (1-209) x AX008791 (1-904)

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Qy 177 SerProAspLysLysLysGlnPheIleGluLysTyAsnPheAspLeuValAsnAsp 196
Db 535 AAA-----CAACTCAAGAAATAATTCAGAGAGAGTACATTTTCGATTTTCGAGAGGAG 588
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DEFINITION Sequence 1 from Patent WO0250292.
ACCESSION AX463060
VERSION AX463060.1 GI:21886074
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
1
AUTHORS Powe, L.C., Wang, H. and Zhou, Y.
TITLE Modulation of plant cyclin-dependent kinase inhibitor activity
JOURNAL Patent: WO 0250292-A 1 27-JUN-2002;
University of Saskatchewan Technologies (CA); Minister of
Agriculture and Agrifood Canada (CA)
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Pred. No.: 4.79e-06 Length: 905
Score: 181.00 Matches: 63
Percent Similarity: 42.24% Conservative: 35
Best Local Similarity: 27.16% Mismatches: 68
Query Match: 17.32% Indels: 66
DB: 6 Gaps: 10

US-09-980-758A-8 (1-209) x AX463060 (1-905)

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Search completed: September 30, 2005, 13:02:26

Job time : 4189 secs

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Qy 132 -----ThrSerProValSerGluGlyLeu----- 139
Db 356 AATCCATCGAGAAATATTATCATCGGAATTTGAATCGCGGTTAAAGAAATCGTTAGATTGT 415
Qy 140 -----GlyGluThrThrGluMetGluSerSerSerAlaThrLysArgLysGln 156
Db 416 TGTGTAGCGGAGGAGAAACGATGGAGAGACGCTGACGGCGGAGGAGGAGGAGGAGCG 475
Qy 157 ProGlyValArgLysThrProThrAlaAlaGluLeuGluAspLeuPheSerGluLeu 176
Db 476 AATTTGATGACGAGATGCCACCGAATCGGAATTTGAAGATTTTTCGAGAGCTGAG 535
Qy 177 SerProAspLysLysLysGlnPheIleGluLysTyAsnPheAspLeuValAsnAsp 196
Db 536 AAA-----CAACTCAAGAAATAATTCAGAGAGAGTACATTTTCGATTTTCGAGAGGAG 589
Qy 197 GluProLeuGluGlyArgTyrLysTrpAspArgLeu 208
Db 590 AAGCCATTAGAGGACGTTACGAATGGTAAAGTTA 625

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PA (HUTC-) HUTCHINSON CANCER RES CENT FRED.

XX Roberts J, Kelly B;

XX WPI; 2001-024998/03.

DR P-PSDB; AAB47001.

XX Functionally inactivating expression of plant D-like cyclin inhibitor  
PT gene for producing a hyperplastic variant plant, modulating the growth  
PT and/or yield of plants, and increasing the proportion of dividing cells.

XX Claim 16; Page 41; 50pp; English.

XX The sequence given in AAC85201 represents a plant D-like cyclin inhibitor  
CC gene, BRO4. This sequence may be used to produce a hyperplastic variant  
CC plant, increase the growth rate of a plant, or increase the proportion of  
CC dividing cells in a plant cell population, relative to a wild-type plant,  
CC by functionally inactivating the expression of a plant D-like cyclin  
CC inhibitor gene in a plant. This sequence is homologous to a sequence  
CC present in a D-like cyclin inhibitor gene and when integrated at the  
CC corresponding locus, functionally inactivates plant D-like cyclin  
CC inhibitor protein expression. BRO4 is useful for producing hyperplastic  
CC variant plants, increasing the growth rate of a plant and for increasing  
CC the proportion of dividing cells in a plant cell population comprising  
CC protoplast, seeds, root cells, meristem cells or leaf cells

XX Sequence 626 BP; 202 A; 131 C; 156 G; 137 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,99e-89 Length: 626  
Score: 1037.00 Matches: 207  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.23% Indels: 0  
DB: 5 Gaps: 0

US-09-980-758A-8 (1-209) x AAC85201 (1-626)

QY 2 ArgAspLeuProLysAsnProArgGluLysLysMetSerGluArgLysArgGluLeuA 21  
DB 3 CGAGATTTCACCAAAATCCAGAGAGAAAAATGAGCGAGAGAAACGAGAGCTTGA 62  
QY 22 GluGluAlaSerSerThrSerPheSerProLeuLysLysThrLysLeuAsnAspSer 41  
DB 63 GAAGAAGCTTCAAGCACAGCTTCTCACCACTGAAGAAACGAGCTTAATGATCTTCT 122  
QY 42 AspSerSerProAspSerHisAspValIleValPheAlaValSerSerSerValAla 61  
DB 123 GATTTCATCCCGGACTCTCATGACGTCATCGTCTTCGCGGTTTCATCTTCTCGT 182  
QY 62 SerSerAlaAlaLeuAlaSerAspGluCysSerValThrIleGlyGluGluSerAsp 81  
DB 183 TCGTCGGCGGCTTTAGCGTCTGATGAATGTTCCGTTTACCATCGGTGGAGAAAGTAT 242  
QY 82 GlnSerSerIleSerSerGlyCysPheThrSerGluSerLysGluIleAlaLysAsn 101  
DB 243 CAGTCCTCGATATCAGCTCCGGTTGTTCCACAGTGAATCGAAGAATCGGAAGAC 302  
QY 102 SerSerSerPheGlyValAspLeuGluAspHisGlnIleGluThrGluThrSer 121  
DB 303 AGTTCTGCTTGGTGTAGATCTGAGGATCATCAAAATCGAAACCGAAACCGAACTCA 362  
QY 122 ThrPheIleThrSerAspPheArgLysGluThrSerProValSerProGluLysGlu 141  
DB 363 ACATTTCATCACAGCAATTCAGAAAAAGAGACGAGTCCAGTGAGTGGGGTTGGAGAA 422  
QY 142 ThrThrThrGluMetGluSerSerSerAlaThrLysArgLysGlnProGlyValArgLys 161  
DB 423 ACGACACAGAAATGGAATCATCATCGCAGCAGAGAGAAACAACCGGGGTGAGGAG 482  
QY 162 ThrProThrAlaAlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAspLys 181  
DB 483 ACTCCACCGGGCGGAGATTGAGGATTGTTCTCGGAGCTAGAGAGTCCAGACGATAAG 542

QY 182 LysLysGlnPheIleGluLysTyrAsnPheAspIleValAsnAspGluProLeuGluGly 201  
DB 543 AAGAGCAATTCATAGAAAAGTACACTTCGATATTGTCAATGACGAACCGCTTGAAGT 602  
QY 202 ArgTyrLysTyrAspArgLeu 208  
DB 603 CGCTACAAGTGGGATCGACTT 623

RESULT 2

AAG29417

ID AAG29417 standard; cDNA; 824 BP.

XX AC AAG29417;

XX DT 29-FEB-2000 (first entry)

XX DE Arabidopsis thaliana CDK inhibitor, ICN2 encoding cDNA.

XX KW Cyclin-Dependent kinase inhibitor; CDK; Interactor of Cyclin 2; ICN2;

XX KW Cdc2a; D-class cyclin; CycD1; CycD2; CycD3; morphogenesis;

XX KW antisense construct; tissue-specific promoter; transgenic plant;

XX KW male sterility; ds.

XX OS Unidentified.

XX FH Key Location/Qualifiers

XX FT CDS 1..639

XX FT /\*tag= a

XX FT /product= "ICN2"

XX PN WO9964599-A1.

XX PD 16-DEC-1999.

XX PF 08-JUN-1999; 99WO-CA000532.

XX PR 08-JUN-1998; 98CA-02235978.

XX PR 31-DEC-1998; 98CA-02256121.

XX PA (MTAC) AGRIC & AGRIFOOD CANADA.

XX PA (UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.

XX PA (CANA) NAT RES COUNCIL CANADA.

XX PI Wang H, Powke LC, Crosby WL;

XX DR WPI; 2000-097540/08.

XX DR P-PSDB; AAY44337.

XX PT Modifying plant cell development using nucleic acid encoding inhibitor of  
PT cyclin-dependent kinase, or corresponding antisense sequence, e.g. for  
PT inducing male sterility.

XX PS Disclosure; Fig 4; 58pp; English.

XX CC The present sequence is a cDNA encoding ICN2 which inhibits A. thaliana  
CC Cyclin-Dependent kinase (CDK). Interactor of Cyclin 2 (ICN2) interacts  
CC with Cdc2a, D-class cyclins, CycD1, CycD2 and CycD3 and shares functional  
CC and sequence similarity with ICK1. Growth, morphogenesis, multiplication,  
CC enlargement, differentiation and maturation of plant cells can be  
CC modified by transforming them with nucleic acid encoding CDK inhibitor or  
CC antisense construct complementary to the inhibitor gene, operably linked  
CC to a tissue-specific promoter. The transgenic plants exhibit alteration  
CC of traits such as petals, male sterility and ability to set seeds

XX SQ Sequence 824 BP; 287 A; 164 C; 185 G; 188 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3e-86 Length: 824  
Score: 1007.00 Matches: 202  
Percent Similarity: 99.51% Conservative: 0  
Best Local Similarity: 99.51% Mismatches: 1  
Query Match: 96.36% Indels: 0

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DB:          3          Gaps:          0
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      28  AAAAAATCCAAGAGAGAAAAAATGACGAGAGAAAGCGAGAGCTTCAGAGAGAGTTCA 87
QY      26  SerThrSerPheSerProLeuLysLysThrLysLeuAsnAspSerSerSerPro 45
      88  AGCACACAGCTTCTCACCACCTGAAGAAACGAAGCTTAATGATTTCTGATTCATCACCG 147
QY      46  AspSerHisAspValIleValPheAlaValSerSerSerValAlaSerSerAlaAla 65
      148  GACTCTCATGACGTATGCTTCGCGGTTTCATCTTCCTTCGCTTCGCGGGCT 207
QY      66  LeuAlaSerAspGluCysSerValThrIleGlyGlyGluSerAspGlnSerSerSer 85
      208  TTAGCGTCTGATGAATGTTCCGTTTACCATCGGTGGAGAGAAAGTGTATGATCCTCGAGT 267
QY      86  IleSerSerGlyCysPheThrSerGluSerLysGluIleAlaLysAsnSerSerPhe 105
      268  ATCAGCTCCGGTGTGTTCCACAGTGAATCGAAAGAAATCGCGAAGAACAGTTCTGCTGTTT 327
QY      106  GlyValAspLeuGluAspHisGlnIleGluThrGluThrGluThrSerThrPheIleThr 125
      328  GGTGTAGATCTGGAGATCATCAATCGAAACCGAAACCGAAACCTCAACATTCATCACCC 387
QY      126  SerAsnPheArgLysGluThrSerProValSerGluGlyLeuGlyGluThrThrGlu 145
      388  AGCAATTTCAAGAAAGACGAGTCCAGTGAGTGGAGGGTTTGGAGAAACGACACAGAA 447
QY      146  MetGluSerSerSerAlaThrLysArgLysGlnProGlyValArgLysThrProThrAla 165
      448  ATGGAATCATATCGCGCAACGAAGAGAAACCAACCGGGGTGAGGAAGACTCCACCGCG 507
QY      166  AlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAspLysLysGlnPhe 185
      508  GCGGAGATTGAGGATTTGTTCTCGGAGCTAGAGAGTCAAGACGATAAAGAAAGCAATTC 567
QY      186  IleGluLysTyrAsnPheAspIleValAsnAspGluProLeuGluGlyArgTyrLysTrp 205
      568  ATAGAAAAGTACAACTTCGATATTGTCATGACGAACCGCTTGAAGGTCGCTACAAAGTG 627
QY      206  AspArgLeu 208
      628  GATCGACTT 636

RESULT 3
AAD40765
ID  AAD40765 standard; cDNA; 824 BP.
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AC  AAD40765;
XX
DT  30-OCT-2002 (first entry)
XX
DE  Arabidopsis thaliana ICN2 cDNA.
XX
KW  plant development; cyclin-dependent kinase; CDK inhibitor; ICN1; ICN2;
KW  ICN2; ICN6; ICN7; ICN8; ICNK; ICNK; morphogenesis; maturation; enlargement;
KW  plant breeding; growth; gene; ss.
XX
OS  Arabidopsis thaliana.
XX
FH  Key
FT  CDS
FT  1..639
FT  /tag= a
FT  /product= "ICN2 protein #1"
FT  /notes= "No start codon"
FT  /partial
FT  49..639
FT  CDS
FT  /tag= b
FT  /product= "ICN2 protein #2"

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XX      WO200250292-A2.
PN      27-JUN-2002.
XX
XX      18-DEC-2001; 2001WO-CA001825.
PF
XX      18-DEC-2000; 2000US-0255908P.
XX
XX      (MIAC ) CANADA MIN AGRIC & AGRI-FOOD CANADA.
PA      (UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.
XX
XX      Wang H, Zhou Y, Fowke LC;
PI      WPI; 2002-519888/55.
XX      P-PSDB; AAE25103, AAE25104.
XX
XX      Modifying plant development, e.g. growth or maturation, which is
XX      particularly useful in plant breeding, by introducing nucleic acids
XX      coding for cyclin-dependent kinase (CDK) inhibitor, cyclin or proteins
XX      that bind to CDK inhibitors.
XX
XX      Disclosure; Fig 4; 89pp; English.
XX
XX      The invention relates to a method for the development of a plant. The
XX      method involves introducing into a plant cell a nucleic acid encoding a
XX      protein that binds or interacts with a cyclin-dependent kinase (CDK)
XX      inhibitor polypeptide (such as ICN1, ICN2, ICN6, ICN7, ICN8 and
XX      ICNK), a cyclin polypeptide, a CDK, or a polypeptide that modulates the
XX      degradation of a CDK inhibitor polypeptide. The method is useful for
XX      modifying the growth and development of plants e.g. morphogenesis,
XX      growth, multiplication, enlargement, differentiation or maturation of a
XX      cell or plant. It is particularly useful in plant breeding. The present
XX      sequence is A. thaliana ICN2 cDNA
XX
SQ      Sequence 824 BP; 287 A; 164 C; 185 G; 188 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:          3e-86          Length:          824
Score:          1007.00          Matches:          202
Percent Similarity: 99.51%          Conservative: 0
Best Local Similarity: 99.51%          Mismatches: 1
Query Match:          96.36%          Indels: 0
DB:          6          Gaps: 0

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QY      6  LysAsnProArgGluLysLysMetSerGluArgLysArgGluLeuAlaGluAlaSer 25
      28  AAAAAATCCAAGAGAGAAAAAATGACGAGAGAAAGCGAGAGCTTCAGAGAGAGTTCA 87
QY      26  SerThrSerPheSerProLeuLysLysThrLysLeuAsnAspSerSerSerPro 45
      88  AGCACACAGCTTCTCACCACCTGAAGAAACGAAGCTTAATGATTTCTGATTCATCACCG 147
QY      46  AspSerHisAspValIleValPheAlaValSerSerSerValAlaSerSerAlaAla 65
      148  GACTCTCATGACGTATGCTTCGCGGTTTCATCTTCCTTCGCTTCGCGGGCT 207
QY      66  LeuAlaSerAspGluCysSerValThrIleGlyGlyGluSerAspGlnSerSerSer 85
      208  TTAGCGTCTGATGAATGTTCCGTTTACCATCGGTGGAGAGAAAGTGTATGATCCTCGAGT 267
QY      86  IleSerSerGlyCysPheThrSerGluSerLysGluIleAlaLysAsnSerSerPhe 105
      268  ATCAGCTCCGGTGTGTTCCACAGTGAATCGAAAGAAATCGCGAAGAACAGTTCTGCTGTTT 327
QY      106  GlyValAspLeuGluAspHisGlnIleGluThrGluThrGluThrSerThrPheIleThr 125
      328  GGTGTAGATCTGGAGATCATCAATCGAAACCGAAACCGAAACCTCAACATTCATCACCC 387
QY      126  SerAsnPheArgLysGluThrSerProValSerGluGlyLeuGlyGluThrThrGlu 145

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Qy	146	MetGluSerSerSerAlaThrLysArgLysGlnProGlyValArgLysThrProThrAla	165
Db	448	ATGGAATCATCATCGGCAACGAGAGAAAACAACCGGGGTGAGAGACTCCAACGGCG	507
Qy	166	AlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAspLysLysGlnPhe	185
Db	508	CGCGAGATTGAGGATTGTTCTCGAGCTAGAGAGTCAAGACGATMAGAAGCAATTC	567
Qy	186	IleGluLysTyrAsnPheAspIleValAsnAspGluProLeuGluGlyArgTyrLysTyr	205
Db	568	ATAGAAAAGTACAACTTCGATATTGTCAATGACGACCGCTTGAAGGTGCTACAAGTGG	627
Qy	206	AspArgLeu	208
Db	628	GATCGACTT	636
RESULT 4			
AAZ29418			
ID	AAZ29418 standard; cDNA; 642 BP.		
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AC	AAZ29418;		
XX			
DT	29-FEB-2000 (first entry)		
XX			
DE	Arabidopsis thaliana CDK inhibitor, ICN6 encoding cDNA.		
XX			
KW	Cyclin-Dependent kinase inhibitor; CDK; Interactor of Cyclin 6; ICN6;		
KW	Cdc2a; D-class cyclin; CycD1; CycD2; CycD3; morphogenesis;		
KW	antennae construct; tissue-specific promoter; transgenic plant;		
KW	male sterility; ds.		
XX			
OS	Unidentified.		
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PR	08-JUN-1998; 98CA-02235978.		
PR	31-DEC-1998; 98CA-02256121.		
XX			
PA	(MIAC ) AGRIC & AGRIFOOD CANADA.		
PA	(UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.		
PA	(CANa ) NAT RES COUNCIL CANADA.		
XX			
PI	Wang H, Fowke LC, Crosby WL;		
XX			
DR	WPI: 2000-097540/08.		
DR	P-PSDB; AAY44338.		
XX			
PT	Modifying plant cell development using nucleic acid encoding inhibitor of		
PT	cyclin-dependent kinase, or corresponding antisense sequence, e.g. for		
PT	inducing male sterility.		
XX			
PS	Disclosure; Fig 5; 58pp; English.		
XX			
CC	The present sequence is a cDNA encoding ICN6 which inhibits A. thaliana		
CC	Cyclin-Dependent kinase (CDK). Interactor of Cyclin 6 (ICN6) interacts		
CC	with Cdc2a, D-class cyclins, CycD1, CycD2 and CycD3 and shares functional		
CC	and sequence similarity with ICK1. Growth, morphogenesis, multiplication,		
CC	enlargement, differentiation and maturation of plant cells can be		
CC	modified by transforming them with nucleic acid encoding CDK inhibitor or		
CC	antisense construct complementary to the inhibitor gene, operably linked		
CC	to a tissue-specific promoter. The transgenic plants exhibit alteration		
CC	of traits such as petals, male sterility and ability to set seeds		



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PR	09-JUL-1999;	99US-0142920P.	PR	28-SEP-1999;	99US-0156458P.
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PR	13-JUL-1999;	99US-0143542P.	PR	04-OCT-1999;	99US-0157117P.
PR	14-JUL-1999;	99US-0143624P.	PR	05-OCT-1999;	99US-0157753P.
PR	15-JUL-1999;	99US-0144005P.	PR	06-OCT-1999;	99US-0157865P.
PR	16-JUL-1999;	99US-0144085P.	PR	07-OCT-1999;	99US-0158029P.
PR	16-JUL-1999;	99US-0144086P.	PR	08-OCT-1999;	99US-0158232P.
PR	19-JUL-1999;	99US-0144325P.	PR	12-OCT-1999;	99US-0158369P.
PR	19-JUL-1999;	99US-0144331P.	PR	13-OCT-1999;	99US-0159293P.
PR	19-JUL-1999;	99US-0144332P.	PR	13-OCT-1999;	99US-0159294P.
PR	19-JUL-1999;	99US-0144333P.	PR	13-OCT-1999;	99US-0159295P.
PR	19-JUL-1999;	99US-0144334P.	PR	14-OCT-1999;	99US-0159329P.
PR	19-JUL-1999;	99US-0144335P.	PR	14-OCT-1999;	99US-0159330P.
PR	20-JUL-1999;	99US-0144352P.	PR	14-OCT-1999;	99US-0159331P.
PR	20-JUL-1999;	99US-0144632P.	PR	14-OCT-1999;	99US-0159637P.
PR	20-JUL-1999;	99US-0144884P.	PR	14-OCT-1999;	99US-0159638P.
PR	21-JUL-1999;	99US-0144814P.	PR	18-OCT-1999;	99US-0159584P.
PR	21-JUL-1999;	99US-0145086P.	PR	21-OCT-1999;	99US-0160741P.
PR	21-JUL-1999;	99US-0145088P.	PR	21-OCT-1999;	99US-0160767P.
PR	22-JUL-1999;	99US-0145085P.	PR	21-OCT-1999;	99US-0160768P.
PR	22-JUL-1999;	99US-0145087P.	PR	21-OCT-1999;	99US-0160770P.
PR	22-JUL-1999;	99US-0145089P.	PR	21-OCT-1999;	99US-0160814P.
PR	22-JUL-1999;	99US-0145192P.	PR	21-OCT-1999;	99US-0160815P.
PR	23-JUL-1999;	99US-0145145P.	PR	22-OCT-1999;	99US-0160980P.
PR	23-JUL-1999;	99US-01452218P.	PR	22-OCT-1999;	99US-0160981P.
PR	23-JUL-1999;	99US-0145224P.	PR	22-OCT-1999;	99US-0160989P.
PR	26-JUL-1999;	99US-0145276P.	PR	25-OCT-1999;	99US-0161404P.
PR	27-JUL-1999;	99US-0145913P.	PR	25-OCT-1999;	99US-0161405P.
PR	27-JUL-1999;	99US-0145918P.	PR	25-OCT-1999;	99US-0161406P.
PR	27-JUL-1999;	99US-0145919P.	PR	26-OCT-1999;	99US-0161359P.
PR	28-JUL-1999;	99US-0145951P.	PR	26-OCT-1999;	99US-0161360P.
PR	02-AUG-1999;	99US-0146388P.	PR	26-OCT-1999;	99US-0161361P.
PR	02-AUG-1999;	99US-0146389P.	PR	28-OCT-1999;	99US-0161920P.
PR	03-AUG-1999;	99US-0147038P.	PR	28-OCT-1999;	99US-0161992P.
PR	04-AUG-1999;	99US-0147204P.	PR	28-OCT-1999;	99US-0161993P.
PR	04-AUG-1999;	99US-0147302P.	PR	29-OCT-1999;	99US-0162142P.
PR	05-AUG-1999;	99US-0147192P.	Alignment Scores:		
PR	05-AUG-1999;	99US-0147260P.	Pred. No.:	7.64e-08	Length:
PR	06-AUG-1999;	99US-0147303P.	Score:	181.00	Matches:
PR	06-AUG-1999;	99US-0147418P.	Percent Similarity:	42.24%	Conservative:
PR	09-AUG-1999;	99US-0147493P.	Best Local Similarity:	27.16%	Mismatches:
PR	09-AUG-1999;	99US-0147935P.	Query Match:	17.32%	Indels:
PR	10-AUG-1999;	99US-0148171P.	DB:	3	Gaps:
PR	11-AUG-1999;	99US-0148319P.	US-09-980-758A-8 (1-209) x AAC36958 (1-780)		
PR	12-AUG-1999;	99US-0148341P.	QY	5	ProLysAsnProArgGluLysLysMetSerGluArgLysArgGluLeuAlaGluAla 24
PR	13-AUG-1999;	99US-0148565P.	Db	21	CCTAAATCGAAGATGGTGAGAAAATATAGAAAAGCTAAA---GGAAITGTAGAACTCGA 77
PR	16-AUG-1999;	99US-0148684P.	QY	25	SerSerThrSerPheSerProLeuLysLysThrLysLeuAsnAspSerSerAspSerSer 44
PR	17-AUG-1999;	99US-0149175P.	Db	78	GTTTCGTCAAGTATATGCAGCTACGAGCCGGAGA----- 113
PR	18-AUG-1999;	99US-0149426P.	QY	45	ProAspSerHisAspValIleValPheAlaValSerSerSerSerValAlaSerSerAla 64
PR	20-AUG-1999;	99US-0149722P.			
PR	20-AUG-1999;	99US-0149723P.			
PR	20-AUG-1999;	99US-0149929P.			
PR	23-AUG-1999;	99US-0149902P.			
PR	23-AUG-1999;	99US-0149930P.			
PR	25-AUG-1999;	99US-0150566P.			



Db 114 -----ATTGTTTATGTAGATCGGAAAAATCA----- 140

QY 65 AlaLeuA1SerHspGluCysSerValThrIleGlyGluCysSerGlnSerSer 84  
 Db 141 -----AGCTCTGTCTCGTCTCGTCA-----AAT 167

QY 85 SerIleSerSerGlyCysPheThrSerGluSerLysGluLeuAlaLysAsnSerSer 104  
 Db 168 GGGATTTCATCGTCTGT-----AGTGGAGCAATGATATTAAGAAAGAAATTA--- 218

QY 105 PheGlyValAspLeuGluAspHisGlnIleGluThrGluThrSerThrPhe--- 123  
 Db 219 -----ATACATCTGGAGGAGGAAGATAAAGATGTGCACACTGAACGTCGCGTATCGA 272

QY 124 -----IleThrSerAsnPheArgLysGlu----- 131

Db 273 CGGGGTACGAAGAGGAAGCTTTTGAATAATCTGAGAGAGGAGGAGAGAAAGAAATTAAGT 332

QY 132 -----ThrSerProValSerGluGlyLeu----- 139

Db 333 AAATCCATGGAGAAATATTATCATCGGAATTTGAATCGCGGTTAAAGAAATCGTTAGATTGT 392

QY 140 -----GlyGluThrThrGluMetGluSerSerSerAlaThrLysArgLysGln 156  
 Db 393 TGTGTGACGGGAGGAGAAACGATCGAGGACGTCGCGCGGAGGAGGAGGAGGCG 452

QY 157 ProGlyValArgLysThrProThrAlaGluIleGluAspLeuPheSerGluLeuGlu 176  
 Db 453 AAATTGATCAGCGAGATGCCACGGAATCGGAATTTGAAGATTTTTTGTGGAAGCTGAG 512

QY 177 SerProAspLysLysGlnPheIleGluLysTyrAsnPheAspLeuValAsnAsp 196  
 Db 513 AAA-----CAACTCAAGAAAGAAATTCAGAGAGAGTACAATTCGATTTCGAGAGAGAG 566

QY 197 GluProLeuGluGlyArgTyrLysTrpAspArgLeu 208  
 Db 567 AAGCCATTAGAGGAGCTTACGATGGGTAAAGTTA 602

RESULT 8  
 AAZ29415  
 ID AAZ29415 standard; cDNA; 904 BP.  
 AC AAZ29415;  
 XX  
 DT 29-FEB-2000 (first entry)  
 XX  
 DE Arabidopsis thaliana CDK inhibitor, ICK1 encoding cDNA.  
 XX  
 KW Cyclin-Dependent kinase inhibitor; CDK; Interactor of Cdc2 kinase 1;  
 KW ICK1; Cdc2a; D-class cyclin; CycD1; CycD2; CycD3; morphogenesis;  
 KW antisense construct; tissue-specific promoter; transgenic plant;  
 KW male sterility; ds.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 FH Key Location/Qualifiers  
 FT misc\_feature 40..42  
 FT /\*tag= c  
 FT /note= "In-frame stop codon"  
 FT CDS 55..630  
 FT /\*tag= a  
 FT /product= "ICK1"  
 FT /replace(318, G)  
 FT /\*tag= b  
 FT /note= "Present in genomic DNA"  
 FT misc\_feature 661..663  
 FT /\*tag= d  
 FT /note= "In-frame stop codon"  
 FT  
 XX WO964599-A1.  
 XX  
 PD 16-DEC-1999.  
 XX

PF 08-JUN-1999; 99WO-CA000532.  
 XX  
 PR 08-JUN-1998; 98CA-02235978.  
 PR 31-DEC-1998; 98CA-02256121.  
 XX  
 PA (MIAC ) AGRIC & AGRIFOOD CANADA.  
 PA (UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.  
 PA (CANA ) NAT RES COUNCIL CANADA.  
 XX  
 PI Wang H, Fowke LC, Crosby WL;  
 XX WPI; 2000-097540/08.  
 DR P-PSDB; AAY44335.  
 XX  
 PT Modifying plant cell development using nucleic acid encoding inhibitor of  
 PT cyclin-dependent kinase, or corresponding antisense sequence, e.g. for  
 PT inducing male sterility.  
 XX  
 PS Claim 5; Fig 1; 58pp; English.  
 XX  
 CC The present sequence is a cDNA encoding A. thaliana Cyclin-Dependent  
 CC kinase (CDK) inhibitor, ICK1. Interactor of Cdc2 kinase 1 (ICK1)  
 CC interacts with Cdc2a, D-class cyclins, CycD1, CycD2 and CycD3. Growth,  
 CC morphogenesis, multiplication, enlargement, differentiation and  
 CC maturation of plant cells can be modified by transforming them with  
 CC nucleic acid encoding CDK inhibitor or antisense construct complementary  
 CC to the inhibitor gene, operably linked to a tissue-specific promoter. The  
 CC transgenic plants exhibit alteration of traits such as petals, male  
 CC sterility and ability to set seeds  
 XX  
 SQ Sequence 904 BP; 307 A; 107 C; 229 G; 261 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 9,22e-08 Length: 904  
 Score: 181.00 Matches: 63  
 Percent Similarity: 42.24% Conservative: 35  
 Best Local Similarity: 27.16% Mismatches: 68  
 Query Match: 17.32% Indels: 66  
 DB: 3 Gaps: 10  
 US-09-980-758A-8 (1-209) x AAZ29415 (1-904)  
 QY 5 ProLysAsnProArgGluLysLysMetSerGluArgLysArgGluLeuAlaGluAla 24  
 Db 43 CCTAAATCGAAGATCGTGAGAAATATAGAAAAGCTAAA---GGAATTGTAGAAGCTGGA 99  
 QY 25 SerSerThrSerPheSerProLeuLysThrLysLeuAsnAspSerSerSerSer 44  
 Db 100 GTTTCGTCACTATATGCTAGCTAGCGCCGAGA----- 135  
 QY 45 ProAspSerHisAspValIleValPheAlaValSerSerSerSerValAlaSerSerAla 64  
 Db 136 -----ATTGTTTATGTAGTACGAAAAATCA----- 162  
 QY 65 AlaLeuAlaSerAspGluCysSerValThrIleGlyGluCysSerGlnSerSer 84  
 Db 163 -----AGCTCTGTCTCGTCTCGTGTAT-----AAT 189  
 QY 85 SerIleSerSerGlyCysPheThrSerGluSerLysGluLeuAlaLysAsnSerSer 104  
 Db 190 GGAATTCGTCTCTCTTGT-----AGTGAACCAATGATATTAAGAAAGAAATTA--- 240  
 QY 105 PheGlyValAspLeuGluAspHisGlnIleGluThrGluThrSerThrPhe--- 123  
 Db 241 -----ATACATCTGGAGGAGGAAGATAAAGATGTGTGACACTGAAACGTCGCGTATCGA 294  
 QY 124 -----IleThrSerAsnPheArgLysGlu----- 131  
 Db 295 CGGGGTACGAAGAGGAAGCTTTTGAATAATCTGAGAGAGGAGGAGAGAAAGAAATTAAGT 354  
 QY 132 -----ThrSerProValSerGluGlyLeu----- 139  
 Db 355 AAATCCATGGAGAAATATTATTCGGAATTTGAATCGCGGTTAAAGAAATCGTTAGATTGT 414

QY 140 -----GlyGluThrThrGluMetGluSerSerAlaThrLysArgLysGln 156  
 Db 415 TGTTCAGCGGAGGAAACGATGAGGAGACGGTCAGCGGAGGAGGAGGAGCG 474  
 QY 157 ProGlyValArgLysThrProThrAlaAlaGluLeuGluAspLeuPheSerGluLeuGlu 176  
 Db 475 AAATTGATGACGAGATGCCAACGGAATCGGAATTTGAAGATTTTGTGGAAGCTGAG 534  
 QY 177 SerProAspAspLysLysGlnPheIleGluLysTyrAsnPheAspIleValAsnAsp 196  
 Db 535 AAA-----CAACTCAAGAAATAATCAAGAGAAGTACAATTCGATTCGAGAAGGAG 588  
 QY 197 GluProLeuGluGlyArgTyrLysTrpAspArgLeu 208  
 Db 589 AAGCCATTAGAGGAGCGTTACGAATGGTAAAGTTA 624

RESULT 9  
 AAD40761  
 ID AAD40761 standard; cDNA; 905 BP.  
 XX  
 AC AAD40761;  
 DT 30-OCT-2002 (first entry)  
 XX  
 DE Arabidopsis thaliana ICK1 cDNA.  
 XX  
 KW Plant development; cyclin-dependent kinase; CDK inhibitor; ICK1; ICK2;  
 KW ICKN6; ICKN7; ICKN8; ICKD; morphogenesis; maturation; enlargement;  
 KW plant breeding; growth; gene; ss.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 56..631  
 FT /\*tag= a  
 FT /product= "ICK1 protein"  
 XX  
 PN WO200250292-A2.  
 XX  
 PD 27-JUN-2002.  
 XX  
 PF 18-DEC-2001; 2001WO-CA001825.  
 XX  
 PR 18-DEC-2000; 2000US-0255908P.  
 XX  
 PA (MIRAC) CANADA MIN AGRIC & AGRI-FOOD CANADA.  
 PA (UUSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.  
 XX  
 PI Wang H, Zhou Y, Fowke LC;  
 XX  
 DR WPI; 2002-519888/55.  
 DR P-PSDB; AAE25101.  
 XX  
 PT Modifying plant development, e.g. growth or maturation, which is  
 PT particularly useful in plant breeding, by introducing nucleic acids  
 PT coding for cyclin-dependent kinase (CDK) inhibitor, cyclin or proteins  
 PT that bind to CDK inhibitors.  
 XX  
 PS Disclosure; Fig 1; 89pp; English.  
 XX  
 CC The invention relates to a method for the development of a plant. The  
 CC method involves introducing into a plant cell a nucleic acid encoding a  
 CC protein that binds or interacts with a cyclin-dependent kinase (CDK)  
 CC inhibitor polypeptide (such as ICK1, ICK2, ICKN2, ICKN6, ICKN7, ICKN8 and  
 CC ICKD), a cyclin polypeptide, a CDK, or a polypeptide that modulates the  
 CC degradation of a CDK inhibitor polypeptide. The method is useful for  
 CC modifying the growth and development of plants e.g. morphogenesis,  
 CC growth, multiplication, enlargement, differentiation or maturation of a  
 CC cell or plant. It is particularly useful in plant breeding. The present  
 CC sequence is A. thaliana ICK1 cDNA  
 XX  
 SQ Sequence 905 BP; 307 A; 107 C; 230 G; 261 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 9, 24e-08 Length: 905  
 Score: 181.00 Matches: 63  
 Percent Similarity: 42.24% Conservatives: 35  
 Best Local Similarity: 27.16% Mismatches: 68  
 Query Match: 17.32% Indels: 66  
 DB: 6 Gaps: 10

US-09-980-758A-8 (1-209) x AAD40761 (1-905)

QY 5 ProLysAsnProArgGluLysLysMetSerGluArgLysArgGluLeuAlaGluGluAla 24  
 Db 44 CCTAAATCGAAGATGCTGAGAAATATAGAAAAGCTAAA---GGAATTTGTAGAACTGGA 100  
 QY 25 SerSerThrSerPheSerProLeuLysLysThrLysLeuAsnAspSerSerAspSerSer 44  
 Db 101 GTTTCGTCAACGTATATGACGTACGAGCCGGAGAG----- 136  
 QY 45 ProAspSerHisAspValIleValPheAlaValSerSerSerSerValAlaSerSerAla 64  
 Db 137 -----ATTGTTTATGTTAGATCGGAAATCA----- 163  
 QY 65 AlaLeuAlaSerAspGluCysSerValThrIleGlyGlyGluGluSerAspGlnSerSer 84  
 Db 164 -----AGCTCTGTCTCCGTCGCGTGAT-----AAT 190  
 QY 85 SerIleSerSerGlyCysPheThrSerGluSerLysGluIleAlaLysAsnSerSerSer 104  
 Db 191 GGAGTTTTCGTCGCTCTTGT-----AGTGAAGCAATGAATATAAGAAAGAAATA--- 241  
 QY 105 PheGlyValAspLeuGluAspHisGlnIleGluThrGluThrGluThrSerThrPhe--- 123  
 Db 242 -----ATACATCTGGAGGAGGAGATAAAGATGGTGACACTGAAACGTCGACGTATCGA 295  
 QY 124 -----IleThrSerAsnPheArgLysGlu----- 131  
 Db 296 CGGGGTACGAAGAGGAGAGCTTTTGAATACTGAGAGAGGAGAGAGAGAAAGAAATTAAGT 355  
 QY 132 -----ThrSerProValSerGluGlyLeu----- 139  
 Db 356 AAATCCATGGAGAATATTATTCATCGGAATTTGAATCGCGGTTAAAGAAATCGTATGATTGT 415  
 QY 140 -----GlyGluThrThrThrGluMetGluSerSerSerAlaThrLysArgLysGln 156  
 Db 416 TGTTCAGCGGAGGAGAAACGATGAGGAGACGGTGACGGCGGAGGAGGAGGAGGCG 475  
 QY 157 ProGlyValArgLysThrProThrAlaAlaGluLeuGluAspLeuPheSerGluLeuGlu 176  
 Db 476 AAATTGATGACGAGATGCCAACGGAATCGGAATTTGAAGATTTTGTGGAAGCTGAG 535  
 QY 177 SerProAspAspLysLysGlnPheIleGluLysTyrAsnPheAspIleValAsnAsp 196  
 Db 536 AAA-----CAACTCAAGAAATAATCAAGAGAAGTACAATTCGATTCGAGAAGGAG 589  
 QY 197 GluProLeuGluGlyArgTyrLysTrpAspArgLeu 208  
 Db 590 AAGCCATTAGAGGAGCGTTACGAATGGTAAAGTTA 625

RESULT 10  
 ADN72202  
 ID ADN72202 standard; cDNA; 630 BP.  
 XX  
 AC ADN72202;  
 XX  
 DT 15-JUL-2004 (first entry)  
 XX  
 DE Thale cress cDNA upregulated in E2Fa/Dpa expressing plants SeqID 97.  
 XX  
 KW gene; ss; plant; transgenic; E2Fa/Dpa transcription factor;  
 KW growth regulator; animal feed product; thale cress;  
 KW cell wall biosynthesis; nitrogen metabolism; carbon metabolism.  
 XX

OS Arabidopsis thaliana.  
 PN WO2004035798-A2.  
 XX 29-APR-2004.  
 XX 20-OCT-2003; 2003WO-EP011658.  
 XX 18-OCT-2002; 2002EP-00079408.  
 XX (CROP-) CROPDESIGN NV.  
 XX Inze D, De Veylder L, Vlieghe K;  
 XX WPI; 2004-348466/32.  
 DR P-PSDB; ADN72203.  
 XX  
 PT Altering plant characteristics, useful for producing plants for enzyme or  
 PT pharmaceutical production comprises modifying in a plant, expression of  
 PT one or more nucleic acids and/or modifying level or activity of one or  
 PT more proteins.  
 XX  
 PS Claim 1; SEQ ID NO 97; 134pp; English.  
 XX  
 CC This invention relates to a novel method for altering one or more plant  
 CC characteristics. Specifically, it refers to identifying genes that are up  
 CC - or down-regulated in transgenic plants overexpressing the heterodimeric  
 CC E2Fa/Dpa transcription factor of Arabidopsis and using these sequences to  
 CC alter plant characteristics accordingly. The present invention describes  
 CC generating transgenic plants for the production of growth regulators,  
 CC enzymes, therapeutics, pharmaceuticals and animal feed products, where  
 CC the altered plant characteristics are selected from increased yield or  
 CC biomass, enhanced survival capacity, stress tolerance, plant architecture  
 CC or physiology, altered endoreduplication, biochemistry, signal  
 CC transduction, storage lipid mobilisation and/or altered photosynthesis,  
 CC each relative to the corresponding wild type plants. Accordingly, these  
 CC sequences can also be useful as positive or negative selectable markers  
 CC during transformation of cells or tissues. The identified genes play a  
 CC role in a variety of biological processes such as DNA replication, cell  
 CC wall biosynthesis, nitrogen and/or carbon metabolism or they function as  
 CC transcription factors. This polynucleotide sequence is thale cress cDNA  
 CC upregulated 1.3 fold or more in plants overexpressing the E2Fa/Dpa  
 CC transcription factor, given in an exemplification of the invention.  
 XX  
 SQ Sequence 630 BP; 191 A; 83 C; 202 G; 154 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1.39e-07 Length: 630  
 Score: 177.00 Matches: 65  
 Percent Similarity: 51.42% Conservative: 44  
 Best Local Similarity: 30.66% Mismatches: 73  
 Query Match: 16.94% Indels: 30  
 DB: 12 Gaps: 13  
 US-09-980-758A-8 (1-209) x ADN72202 (1-630)  
 QY 16 ArgLysArgGluLeuAlaGluAlaSerSerThrSerPheSerProLeuLysIysThr 35  
 Db 19 AGAAGACGAGATGTGGTTGAAGAGAAATGAGTACGACG---ACGACGGTGAACACGAAG 75  
 QY 36 LysLeuAsnAspSerSerAspSerProAspSerHisAspValIleValPheAlaVal 55  
 Db 76 AAGATCGAGGAGGAGTGGAT---TTAGTGAATCTAGGATTAATCTCTCGTGTGTA 132  
 QY 56 SerSerSerSer-----ValAlaSerSerAlaAlaLeuAlaSerAspGluCys 71  
 Db 133 CAGCGCAGCAATCGCGTGAATTTGGCGAGAAATTCAGCAGGACGTCGGAGACGAT 192  
 QY 72 SerValThrIleGlyGlyGluGluSer-----Asp 81  
 Db 193 GTTGTATTAGTAGCAGCGCAGGATCTCTCCGGTTGAAGACAGTGTCAATTCGAAGAA 252  
 QY 82 GlnSerSerSerIleSerSerGlyCysPheThrSerGluSerLysGluIleAlaLysAsn 101

Db 253 GAAGATTCTCGTGGTTTCGGTGT---TGTTCTATCGAAGAGAAA-----TCGAACCG 303  
 QY 102 SerSerSerPheGlyValAspLeuGluAspHisGln---IleGluThrGluThrGluThr 120  
 Db 304 AGAATCGAATTT---GTAGATCTTGAGGAAATAACGGTCAGCATCGTGAACAGAAACG 360  
 QY 121 SerThrPheIleThrSerAsnPheArgLysGluThrSerProValSerGluGlyLeuGly 140  
 Db 361 TCG---TGGATTACGATGATTTGAATAAG-----AGTCAGGAATCGATGAACATGGAT 411  
 QY 141 GluThrThrThrGluMetGluSerSerSerAlaThrLysArgLysGlnProGlyValArg 160  
 Db 412 TCTTCTTCGGTGGCTGTTGAAGATGTAGAGTCTCGCCGAGGTAAAGAGAGACTTCCAT 471  
 QY 161 LysThrProThrAlaAlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAsp 180  
 Db 472 GAGACGGTGAAGAAAGCTGAGTTAGAAGACTTTTTTCAGGTGGCGGAGAAA-----GAT 525  
 QY 181 LysLysLysGlnPheIleGlu-----LysTyrAsnPheAspIleValAsnAspGlu 197  
 Db 526 CTTCGAATAAGTTGTTGGAATGTTCTATGAAGTATACTTCGATTTCGAGAAAGATGAG 585  
 QY 198 ProLeu---GluGlyArgTyrLysTyrAspArgLeu 208  
 Db 586 CCACCTTGGTGGAGGAATACGATGCGGTAAATTG 621  
 RESULT 11  
 AAC85204  
 ID AAC85204 standard; DNA; 809 BP.  
 AC AAC85204;  
 XX 22-MAR-2001 (first entry)  
 DE Plant D-like cyclin inhibitor BRO3 coding sequence.  
 XX  
 KW Plant; D-like cyclin inhibitor gene; BRO4; hyperplastic; variant;  
 KW growth rate; dividing cells; inactivation; protoplast; seed; root cell;  
 KW meristem; leaf; ss.  
 XX Arabidopsis thaliana.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 CDS 69..620  
 FT /\*tag= a  
 FT /product= "BRO3"  
 FT  
 XX WO2000069883-A1.  
 XX 23-NOV-2000.  
 XX 15-MAY-2000; 2000WO-US013379.  
 XX 14-MAY-1999; 99US-0134373P.  
 XX (HUTC-) HUTCHINSON CANCER RES CENT FRED.  
 XX Roberts J, Kelly B;  
 XX WPI; 2001-024998/03.  
 DR P-PSDB; AAB47004.  
 XX  
 PT Functionally inactivating expression of plant D-like cyclin inhibitor  
 PT gene for producing a hyperplastic variant plant, modulating the growth  
 PT and/or yield of plants, and increasing the proportion of dividing cells.  
 XX  
 PS Example 1; Page 39-40; 50pp; English.  
 XX  
 CC The sequence given in AAC85204 represents a plant D1 cyclin inhibitor  
 CC gene, BRO3. This sequence was isolated using a yeast two hybrid screen.  
 CC The BRO3 protein was found to contain a seven amino acid sequence cyclin  
 CC binding domain similar to that of BRO1, BRO2 and BRO4 (See also AAB47005-

6). This sequence is homologous to a sequence present in a D-like cyclin inhibitor gene and when integrated at the corresponding locus, functionally inactivates plant D-like cyclin inhibitor protein expression. The BRO4 coding sequence may be used to produce a hyperplastic variant plant, increase the growth rate of a plant, or increase the proportion of dividing cells in a plant cell population, relative to a wild-type plant, by functionally inactivating the expression of a plant D-like cyclin inhibitor gene in a plant. BRO4 is useful for increasing the proportion of dividing cells in a plant cell population comprising protoplast, seeds, root cells, meristem cells or leaf cells

XX  
SQ Sequence 809 BP; 268 A; 110 C; 213 G; 218 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 1,92e-07 Length: 809  
Score: 177.00 Matches: 68  
Percent Similarity: 49.12% Conservative: 43  
Best Local Similarity: 30.09% Mismatches: 73  
Query Match: 16.94% Indels: 42  
DB: 5 Gaps: 14

US-09-980-758A-8 (1-209) x AAC85204 (1-809)

QY 2 ArgAspLeuProLysAsnProArgGluLysLysMetSerGluArgLysGluLeuAla 21  
DB 3 CGAGATTACCA-----CGAGATGTGTT 26

QY 22 GluGluAlaSerSerThrsSerPheSerProLeuLysLysThrsLysLeuAsnAspSerSer 41  
DB 27 GAAGAGAATGGAGTTACGACG---ACGACGGTGAACGAAGAGATGGAGGAGGAAGTG 83

QY 42 AspSerSerProAspSerHisAspValIleValPheAlaValSerSerSerSer----- 59  
DB 84 GAT-----TTAGTGAATCTAGGATAATCTCTCGTGTGTACAGCGACCAATCGCGT 140

QY 60 -----ValAlaSerSerAlaAlaLeuAlaSerAspGluCysSerValThrIleGlyGly 77  
DB 141 GGAATTGTGGGAGAAATTCAGCAGGAGCGTCGGAGACGAGTGTGTTATTAGTAGCAGCG 200

QY 78 GluGluSer-----AspGlnSerSerSerIleSer 87  
DB 201 CGAGATTCCTCCGTTGAAGAACAGTGTCAAAATCGAAGAGAGATTCGTCGTTTCG 260

QY 88 SerGlyCysPheThrsSerSerLysLysGluIleAlaLysAsnSerSerSerPheGlyVal 107  
DB 261 TGT-----TGTTCTACATCGAAGAGAAA-----TCGAAACGGAGATCGAATTT---GTA 308

QY 108 AspLeuGluAspHisGln---IleGluThrGluThrGluThrSerThrPheIleThrSer 126  
DB 309 GATCTTGAGGAAAATAACGGTGACGATCGTGAACACAGAAACGTCG---TGGATTTACGAT 365

QY 127 AsnPheArgLysGluThrSerProValSerGluGlyLeuGlyGluThrThrGluMet 146  
DB 366 GATTTGAATAAG-----AGTGAGGAATCGATGGAACATGGAATCTCTTCGTGGCTGTT 419

QY 147 GluSerSerSerAlaThrLysArgLysGlnProGlyValArgLysThrProThrAlaAla 166  
DB 420 GAAGATGTAGAGTCTCGCGCAGGTTAAGGAAGAGTCTCCATGACCGGTGAAGAAAGCT 479

QY 167 GluIleGluAspLeuPheSerGluLeuGluSerProAspLysLysLysGlnPheIle 186  
DB 480 GAGTTAGAAGACTTTTTCAGGTGCGCGGAGAAA-----GATCTTCGGAATAAGTTGTG 533

QY 187 Glu-----LysTyrAsnPheAspIleValAsnAspGluProLeu---GluGlyArg 202  
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QY 203 TyrLysTyrAspArgLeu 208  
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ID AAD40770 standard; cDNA; 861 BP.  
AC AAD40770;  
XX  
DT 30-OCT-2002 (first entry)  
XX  
DE Arabidopsis thaliana ICK2 full-length cDNA.  
XX  
KW Plant development; cyclin-dependent kinase; CDK inhibitor; ICK1; ICK2;  
KW ICK2; ICK6; ICK7; ICK8; ICK9; ICK10; ICK11; ICK12; ICK13; ICK14;  
KW plant breeding; growth; gene; ss.  
XX  
OS Arabidopsis thaliana.  
XX  
FH Key Location/Qualifiers  
FT CDS 7..636  
FT /\*tag= a  
FT /product= "ICK2 full-length protein"  
XX  
PN WO200250292-A2.  
XX  
PD 27-JUN-2002.  
XX  
PF 18-DEC-2001; 2001WO-CA001825.  
XX  
PR 18-DEC-2000; 2000US-0255908P.  
XX  
PA (MTAC ) CANADA MIN AGRIC & AGRI-FOOD CANADA.  
XX  
FA (UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.  
XX  
PI Wang H, Zhou Y, Fowke LC;  
XX  
DR WPI; 2002-519888/55.  
XX  
DR P-PSDB; AAE25110.  
XX  
PT Modifying plant development, e.g. growth or maturation, which is  
PT particularly useful in plant breeding, by introducing nucleic acids  
PT coding for cyclin-dependent kinase (CDK) inhibitor, cyclin or proteins  
PT that bind to CDK inhibitors.  
XX  
PS Disclosure; Fig 3B; 89pp; English.  
XX  
CC The invention relates to a method for the development of a plant. The  
CC method involves introducing into a plant cell a nucleic acid encoding a  
CC protein that binds or interacts with a cyclin-dependent kinase (CDK)  
CC inhibitor polypeptide (such as ICK1, ICK2, ICK6, ICK7, ICK8 and  
CC ICK9), a cyclin polypeptide, a CDK, or a polypeptide that modulates the  
CC degradation of a CDK inhibitor polypeptide. The method is useful for  
CC modifying the growth and development of plants e.g. morphogenesis,  
CC growth, multiplication, enlargement, differentiation or maturation of a  
CC cell or plant. It is particularly useful in plant breeding. The present  
CC sequence is A. thaliana ICK2 full-length cDNA  
XX  
SQ Sequence 861 BP; 266 A; 114 C; 230 G; 251 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 2,08e-07 Length: 861  
Score: 177.00 Matches: 65  
Percent Similarity: 51.42% Conservative: 44  
Best Local Similarity: 30.66% Mismatches: 73  
Query Match: 16.94% Indels: 30  
DB: 6 Gaps: 13

US-09-980-758A-8 (1-209) x AAD40770 (1-861)

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DB 25 AGAGAACGAGATGTGTTGAAGAGAAATCGAGTTACGACG---ACGACGGTGAACGAAGG 81

QY 36 LysLeuAsnAspSerSerSerSerSerSerProAspSerHisAspValIleValPheAlaVal 55  
DB 82 AAGATGGAGGAGGAAGTGGAT---TTAGTGAATCTAGGATAATTTCTCTCCGTGTGTA 138

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QY 56 SerSerSerSer-----ValAlaSerSerAlaAlaLeuAlaSerAspGluCys 71
DB 139 CAGGCGACGAATCGCGGTGGAATTTGGCGAGAAATTCAGCAGGACGCGTCGAGACGAGT 198
QY 72 SerValThrIleGlyGlyGluGluSer-----Asp 81
DB 199 GTTGTATTAGTACGACGCGGCGGATCTCTCCGGTTGAAGACAGTGTCMAATCGAAGAA 258
QY 82 GlnSerSerSerIleSerSerGlyCysPheThrSerGluSerLysGluLeuAlaLysAsn 101
DB 259 GAAGATTCTCGGTTTCGTGT---TGTTCTACATCGGAAGAGAAA-----TCGAAACGG 309
QY 102 SerSerSerPheGlyValAspLeuGluAspHisGln---IleGluThrGluThrGluThr 120
DB 310 AGAATCGAATTT---GTAGATCTTGAGGAATAAATACGGTGCAGATCGTGGAACACAGAAACG 366
QY 121 SerThrPheIleThrSerAsnPheArgLysGluThrSerProValSerGluGlyLeuGly 140
DB 367 TCG---TCGATTACGATGATTTGATATAG-----AGTCAGGATCGATGACATGGAT 417
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DB 418 TCTTCTTCGGTGGCTGTTCAAGATGTAGAGTCTCGCCGAGGTAAAGGAAGAGTCTCCAT 477
QY 161 LysThrProThrAlaAlaGluLeuGluAspLeuPheSerGluLeuGluSerProAspAsp 180
DB 478 GAGACGGTGAAGGAAGCTAGTTAGAAGACTTTTTTCAGGTGCGCGAGAAA-----GAT 531
QY 181 LysLysLysGlnPheIleGlu-----LysTyrAsnPheAspIleValAsnAspGlu 197
DB 532 CTTCCGAATAAGTTGTTGAAGTGTCTATGAAGTATTACTTCGATTCGAGAAAGATGAG 591
QY 198 ProLeu---GluGlyArgTyrLysTrpAspArgLeu 208
DB 592 CCACCTTGGTGGAGGAAGATACGAGTGGGTAAATTTG 627

RESULT 13
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ID AAC45711 standard; DNA; 883 BP.
XX
XX AAC45711;
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AC AAC45711;
DT 18-OCT-2000 (first entry)
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DE
DE Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
XX Arabidopsis thaliana.
OS
OS EP1033405-A2.
PN
PN
PD
PD 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
XX
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XX 23-MAR-1999; 99US-0125788P.
XX 25-MAR-1999; 99US-0126264P.
XX 29-MAR-1999; 99US-0126785P.
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XX 06-APR-1999; 99US-0128234P.
XX 08-APR-1999; 99US-0128714P.
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XX AC AAC37798;  
XX DT 17-OCT-2000 (first entry)  
XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 18698.  
XX KW Hybridization assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway; metabolic pathway;  
KW promoter; termination sequence; ss.  
XX OS Arabidopsis thaliana.  
XX PN EP1033405-A2.  
XX PD 06-SEP-2000.  
XX PF 25-FEB-2000; 2000EP-00301439.  
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Pred. No.: 2,166-07  
Score: 177.00  
Percent Similarity: 51.4%  
Best Local Similarity: 30.6%  
Query Match: 16.94%  
DB: 3  
Length: 886  
Matches: 65  
Conservative: 44  
Mismatches: 73  
Indels: 30  
Gaps: 13

US-09-980-758A-8 (1-209) x AAC37798 (1-886)

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Db 126 AGAGAACGAGATGTGTTGAGAGAAATGAGTTACGACG---ACGACGTGAACGAAGG 182
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QY 56 SerSerSerSer-----ValAlaSerSerAlaAlaLeuAlaSerAspGluCys 71
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QY 72 SerValThrIleGlyGluGluSer-----Asp 81
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Db 468 TCG---TGGAATTCAGCATGATTTCATAAG-----AGTGAGGAATCGATGAACATGAT 518
QY 141 GluThrThrThrGluMetGluSerSerSerAlaThrLysArgLysGlnProGlyValArg 160
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QY 161 LysThrProThrAlaAlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAsp 180
Db 579 GAGACGCTGAAGGAACTGAGTTAGAAAGATTTTTTTCAGGTGGCGGAGAAA-----GAT 632
QY 181 LysLysLysGlnPheIleGlu-----LysTyrAsnPheAspIleValAsnAspGlu 197
Db 633 CTTCGGAATAAGTTGTTGGAATGTTCTATGAGTATAACTTCGATTTTCGAGAAAGATGAG 692
QY 198 ProLeu---GluGlyArgTyrLysTrpAspArgLeu 208
Db 693 CCACTTGTGTGAGGAAGATACGAGTGGGTTAAATTG 728
RESULT 15
AAAX25015 standard; cDNA; 932 BP.
AC AAAX25015;
XX 05-JUL-1999 (first entry)
XX Arabidopsis cyclin-dependent kinase inhibitor FL39 cDNA clone.
DE Arabidopsis cyclin-dependent kinase inhibitor; CDK inhibitor; CKI; FL39;
KW Cyclin-dependent kinase inhibitor; CDK inhibitor; CKI; CDKI; FL39;
KW plant development; transgenic plant; cell cycle; growth regulator;
KW herbicide; ds.
XX Arabidopsis thaliana.
XX Key Location/Qualifiers
XX CDS 86..715
XX misc_feature 305..932
XX FT /*tag= a
XX FT /*tag= c
XX FT /note= "this region of the sequence is specifically
XX FT claimed in Claim 1(c)"
XX FT polyA_signal 915..920
XX FT /*tag= b
XX PN WO9914331-A2.
XX 25-MAR-1999.
XX 16-SEP-1998; 98WO-EP005895.
XX 16-SEP-1997; 97EP-00202838.
```



PR 24-DEC-1997; 97EP-00204111.  
 XX (CROP-) CROPDISEGN NV.  
 XX Inze D, De Veylder L, De Almeida J, Landrieu I;  
 DR WPI; 1999-229535/19.  
 DR P-PSDB; AAW98179.  
 XX  
 PT DNA encoding inhibitor of cyclin-dependent kinase.  
 XX  
 PS Claim 1b; Page 72-74; 88pp; English.  
 XX  
 CC This is the DNA sequence of FL39, a cDNA clone that encodes a new cyclin-  
 CC dependent kinase (CDK) inhibitor (see AAW98179) of Arabidopsis thaliana.  
 CC New plant products with a putative CDK inhibitory function were screened  
 CC by using a two-hybrid system with CDC2aAT protein as bait and a library  
 CC made from an RNA mixture of A. thaliana cell suspensions harvested at the  
 CC early exponential, exponential, early stationary and stationary phases.  
 CC Positive clones LDV39, LDV66 and LDV159 were obtained. Clone FL39 was  
 CC isolated from a flower cDNA library using partial clone LDV39 as probe.  
 CC Clone FL66 (see AAX25016) was similarly obtained using LDV66. Another CDK  
 CC inhibitor, ALFCDKI (see AAX25018), was obtained from alfalfa. Results  
 CC established that several CDK inhibitors exist in plants and that these  
 CC inhibitors are expressed at different time points and may have different  
 CC functions during the development of the plant. CDK inhibitors, nucleic  
 CC acids, antibodies, promoter sequences, related recombinant DNA and  
 CC vectors are all useful: for diagnosis (no details); for modulating the  
 CC cycle, division and/or growth of plant cells; for altering activity of  
 CC CDK; for modulating growth inhibition in plants caused by environmental  
 CC stress; for inducing male or female sterility; for altering cell division  
 CC progression in plants, bacteria, fungi, insect and animal cells; and to  
 CC screen for agonists or antagonists that are potentially useful as growth  
 CC regulators or herbicides. Plants of any sort can be treated, e.g. to  
 CC alter their size or resistance to disease  
 XX  
 SQ Sequence 932 BP; 289 A; 125 C; 254 G; 264 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 2.3e-07 Length: 932  
 Score: 177.00 Matches: 65  
 Percent Similarity: 51.42% Conservative: 44  
 Best Local Similarity: 30.66% Mismatches: 73  
 Query Match: 16.94% Indels: 30  
 DB: 2 Gaps: 13

US-09-980-758A-8 (1-209) x AAX25015 (1-932)

QY 16 ArgLysArgGluLeuAlaGluGluAlaSerSerThrSerPheSerProLeuLysLysThr 35  
 DB 104 AGAGAACGAGATGCTGGTGAAGAGAGATGGAGTTACGACG---ACGACGGTGAACGAGG 160  
 QY 36 LysLeuAsnAspSerSerSerProAspSerHisAspValIleValPheAlaVal 55  
 DB 161 AAGATGGAGGAGGAAGTGGAT---TTAGTGGAACTAGGATATCTCTCGTGTGTA 217  
 QY 56 SerSerSerSer-----ValAlaSerAlaAlaLeuAlaSerAspGluCys 71  
 DB 218 CAGCGCAGCAATCGCGGTGAATTTGGCGAGAAATTCAGCAGGACGTCGGAGACGAGT 277  
 QY 72 SerValThrIleGlyGluGluSer-----Asp 81  
 DB 278 GTTGTATTAGTACGACGGCGGATCTCTCCGGTTGAAGAACAGTGTCAAAATCGAAGAA 337  
 QY 82 GlnSerSerSerIleSerGlyCysPheThrSerGluSerLysGluIleAlaLysAsn 101  
 DB 338 GAAGATTCGTCGGTTCGTGT---TGTTCTACATCGAAGAGAAA-----TCGAAACGG 388  
 QY 102 SerSerSerPheGlyValAspLeuGluAspHisGln---IleGluThrGluThrGluThr 120  
 DB 389 AGAATCGAATTT---GTAGATCTTTAGAGAAATAACGGTCAGCATCGTGAACAGAAACG 445  
 QY 121 SerThrPheIleThrSerAsnPheArgLysGluThrSerProValSerGluGlyLeuGly 140

Db 446 TCG---TGGATTACGATGATTGTAATAAG-----AGTGAGGAATCGATGAACATGGAT 496  
 QY 141 GluThrThrThrGluMetGluSerSerAlaThrLysArgLysGlnProGlyValArg 160  
 Db 497 TCTTCTCGTGGCTGTTGAAGATGTAGAGTCTCGCGCAGGTAAAGGAAGAGTCTCCAT 556  
 QY 161 LysThrProThrAlaAlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAsp 180  
 Db 557 GAGACGGTGAAGAAAGCTGAGTTAGAAGATTTTTTTCAGTGGCGGAGAAA-----GAT 610  
 QY 181 LysLysLysGlnPheIleGlu-----LysTyrAsnPheAspIleValaAsnAspGlu 197  
 Db 611 CTTCCGAATAGTTGTTGGAATGTTCTATGAAGATATACTTCGATTTCCGAGAAAGATGAG 670  
 QY 198 ProLeu---GluGlyArgTyrLysTrpAspArgLeu 208  
 Db 671 CCACTTGGTGGAGGAAGATACGAGTGGTGAATTTG 706

Search completed: September 30, 2005, 11:52:35  
 Job time : 536 secs

**This Page Blank (uspto)**

**Qy**

16 ArgLysArgGluLeuAlaGluGluAlaSerThrSerPheSerProLeuLysLysThr 35  
|||||::||:::||::|  
**Db**

104 AGAAGAACGAGATGTGGTGAAGAAGAAATTGGAGTTACGACG---ACGACCGTGAAACGCAAGG 160  
|||||::||:::||::|

```
Qy 36 LysLeuAsnAspSerSerAspSerSerProAspSerHisAspValIleValPheAlaVal 55
|||
Db 161 AAGATGGAGGAGGAAGTGGAT--TTAGTGGAAATCTAGATAATCTCTCGGTGCTA 217
|||
Qy 56 SerSerSerSer-----ValIleSerSerAlaAlaLeuAlaSerAspGluCys 71
|||
Db 218 CAGGCGACGAATCGCGGTGGAAATTTGGCGAGAAATTCAGCAGGAGCGTCGAGACACJAGT 277
|||
Qy 72 SerValThrIleGlyGlyGluGluSer-----Asp 81
|||
Db 278 GTTGTTATAGTACGAGCGGAGATCTCTCCGGTTGAAGACACAGTGAATCGAAGAA 337
|||
Qy 82 GlnSerSerSerIleSerSerGlyCysPheThrSerGluSerLysGluIleAlaLysAsn 101
|||
Db 338 GAAGATTCGTGCGTTTCGTGT--TGTTCTACATCGGAAGAGAAA-----TCGAACGG 388
|||
Qy 102 SerSerSerPheGlyValAspLeuGluAspHisGln-----IleGluThrGluThrGluThr 120
|||
Db 389 AGAATCGAATTTT--GTAGATCTTGAGGAAATAACGGGTGACGATCGTGAAACAGAAACG 445
|||
Qy 121 SerThrPheIleThrSerAsnPheArgLysGluThrSerProValSerGluGlyLeuGly 140
|||
Db 446 TCG--TGATTTACGATGATTTGAATAG-----AGTGAGGAATCGATGAACATGGAT 496
|||
Qy 141 GluThrThrThrGluMetGluSerSerAlaThrLysArgLysGlnProGlyValArg 160
|||
Db 497 TCTTCTCGGTGCGTGTGAAGATGATAGACTCCCGCAGGTTAAGGAAGATCTCCAT 556
|||
Qy 161 LysThrProThrAlaAlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAsp 180
|||
Db 557 GAGACGGTGAAGGAAGCTGAGTTAGAAGATTTTTTTCAGGTGGCGGAGAAA-----GAT 610
|||
Qy 181 LysLysLysGlnPheIleGlu-----LysTyrAsnPheAspIleValAsnAspGlu 197
|||
Db 611 CTTCCGAATAAGTTGTTGAATGTTCTATGAAGTATACTTCGATTCGAGAAAGATGAG 670
|||
Qy 198 ProLeu--GluGlyArgTyrLysTyrAspArgLeu 208
|||
Db 671 CCACCTGGTGAGGAGAGATACGAGTGGGTAAATTG 706
|||
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## RESULT 2

```
US-09-526-597D-3
; Sequence 3, Application US/09526597D
; Patent No. 6710227
; GENERAL INFORMATION:
; APPLICANT: De Veylder, Lieven
; APPLICANT: De Almeida, Janice
; APPLICANT: Landrieu, Isabelle
; TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof
; FILE REFERENCE: 1187-2
; CURRENT APPLICATION NUMBER: US/09/526,597D
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 875
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (11)..(658)
US-09-526-597D-3
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Alignment Scores:
Pred. No.: 3.44e-08 Length: 875
Score: 153.00 Matches: 62
Percent Similarity: 42.80% Conservative: 39
Best Local Similarity: 26.27% Mismatches: 73
Query Match: 14.64% Indels: 62
DB: 11 Gaps: 11
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US-09-980-758A-8 (1-209) x US-09-526-597D-3 (1-875)

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Qy 9 ArgGlyLysLysMetSerGluArgLysArgGluLeuAlaGluAlaSerSerThrSer 28
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Db 5 CGAGAGAAATCAAAAGATAAAGTGGCGATATCAGCGCTCATGGAAGTCTCTAAAGCAACAGCT 64
|||
Qy 29 PheSerProLeuLysLysThrLysLeuAsnAspSerSerAspSerSerProAspSerHis 48
|||
Db 65 CCAAGTCCAGGTGTTCCAGAACCGA-----GCCGCT 94
|||
Qy 49 AspValIleValPheAlaValSerSerSerValAlaSerSerAlaAlaLeuAlaSer 68
|||
Db 95 AAACCCCTAGCTTGAAGCGCTTAATCTCCCGCGCTGATTCAGCTCTACCTAACGAC 154
|||
Qy 69 AspGluCysSerValThrIleGlyGlyGluGluSerAspGlnSerSerIle-----86
|||
Db 155 TCTTCTTGCTATCTTCAGTCCGTAGCGCGCTCTCGAGAAACCCCTCTCTCGCTGATGAA 214
|||
Qy 87 -----SerSerGlyCysPheThrSerGluSerLysGlu---97
|||
Db 215 CCGAAACAGCGCCGAGAGTTACAGATCGGGAATTAAGAGTCTGGTTCAGGTCGCG 274
|||
Qy 98 -----IleAlaLysAsnSerSer-----103
|||
Db 275 GTTGACTCGGTAACTCGGTCTCTGAGTCAGAGCTCTAATGAAGATGAATGTTTTCAC 334
|||
Qy 104 -----SerPheGlyValAspLeuGluAspHisGlnIleGluThrGluThr 120
|||
Db 335 AATTTCTGAGTGTCCCAAGTTTCTTGTTGGTGAACAGTCTCGGTTTGAATCAAGACAC 394
|||
Qy 121 SerThrPheIleThrSerAsnPheArgLysGluThrSerProValSer-----GluGly 138
|||
Db 395 AGCACA-----AGGAGAGCAGCGCTTGTAACTTTGTTGAGGAT 433
|||
Qy 139 Leu-----GlyGluThrThrThrGluMetGluSerSerSerAlaThr 152
|||
Db 434 ATGAGATCATGTTACACAGGCTCTAGCAGGAGTCTGATG-----TCGAGAGCAACC 487
|||
Qy 153 Lys-----ArgLysGlnProGlyValArgLysThrProThrAlaAlaGluIleGlu 169
|||
Db 488 AAGAGGTACACAAGGGAACAAGATAACGTG-----ATCCGACCACTAGTGAATGGAG 541
|||
Qy 170 AspLeuPheSerGluLeuGluSerProAspAspLysLysGlnPheIleGluLysTyr 189
|||
Db 542 GAGTTCTTTGCATATGCAGAG-----CAGCAGCAACAGAGGCTATTTCATGGAAGATAC 595
|||
Qy 190 AsnPheAspIleValAsnAspGluProLeuGluGlyArgTyrLysTyr 205
|||
Db 596 AACTTCGACATTGTGAATGATATCCCTCTCAGCGGAGCTTACGAATGG 643
|||
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## RESULT 3

```
US-09-526-597D-5
; Sequence 5, Application US/09526597D
; Patent No. 6710227
; GENERAL INFORMATION:
; APPLICANT: De Veylder, Lieven
; APPLICANT: De Almeida, Janice
; APPLICANT: Landrieu, Isabelle
; TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof
; FILE REFERENCE: 1187-2
; CURRENT APPLICATION NUMBER: US/09/526,597D
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 1193
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (92)..(763)
US-09-526-597D-5
Alignment Scores:
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Pred. No.: 4.56e-06 Length: 1193
Score: 136.50 Matches: 54
Percent Similarity: 43.04% Conservative: 45
Best Local Similarity: 23.48% Mismatches: 82
Query Match: 13.06% Indels: 49
DB: 4 Gaps: 10

US-09-980-758A-8 (1-209) x US-09-526-597D-5 (1-1193)

QY 11 LysLysMetSerGluArgLysArgGluLeuAlaGluAlaSerSerThrSerPheSer 30
Db 116 AAATCCAAATCAGAAATCTCTTCCACCAATTCACACCAACACCAATCACCACCATCA 175
QY 31 ProLeuLysLysThrLysLeuAsnAspSerSerAspSerSerProAspSerHisAspVal 50
Db 176 CCAACCAATCACC---ACCNAATTCACCAACCAACCAACCAACCAATCTCTGATGGT 232
QY 51 Ile-----ValPheAlaValSerSerSer----- 58
Db 233 GTTCGAACTCGTCTAGAACCTAGCTTTGGAGAAATTCACCAATCAGAAATCAGATCTT 292
QY 59 SerValAlaSerSerAla-----AlaLeuAla 67
Db 293 TCTGTTCTTCTGATCTTACCTTACCTGAGGAACGCTCGCTTAAGAGACCCCTTAATT 352
QY 68 SerAspGluCysSerValThrIleGlyGlyGluSerAspGlnSerSerSerIleSer 87
Db 353 AGCAACATTCCTGCTAAGAGGAATAAGGGCATGATGGAACCCCTAAATCCCAATT--- 409
QY 88 SerGlyCysPheThrSerGluSerLysGluLeuAlaLysAsnSerSerPheGlyVal 107
Db 410 ---GGGATTAATTCGTTGAAGAGAAACTGTTGAGAGAGTCTGAGCCCTGAAATGCT 466
QY 108 AspLeuGluAspHisGlnIleGluThrGluThrGluThrSerThrPheIleThrSerAsn 127
Db 467 GAATTCAGAGAGAACTGTGAGGATACTGTAGAGAGCGCT----- 505
QY 128 PheArgLysGluThrSerProVal-----SerGluGlyLeuGlyGlu--- 141
Db 506 ---AGGAAACTACACCCGCTCCATTTGATATGCGAGCAGACGCTTCTCAGGCTCTCT 559
QY 142 ---ThrThrThrGluMetGluSerSerSerAlaThrLysArgLysGlnProGly 158
Db 560 AGCCCAATACAGGCGTACTTTCCAACTGAAGCTAATCCCAAAACGGAGAGCCCACT 619
QY 159 ValArgLysThrProThrAlaAlaGluIleGluAspLeuPheSerGluLeuGluSerPro 178
Db 620 ATC-----CCAAATTCACGCGAATTTGAGGAATTCGTGCTAAACATGAAGCC--- 667
QY 179 AspAspLysLysLysGlnPheIleGluLysTyAsnPheAspIleValAsnAspGluPro 198
Db 668 ---GAGCAGCAAAAGGAGTTTCATGGAGAGTACAACCTTTGATCCTGTGACAGAGCCCA 724
QY 199 LeuGluGlyArgTyLysTrpAspArgLeu 208
Db 725 CTCCAGGGCGTTACGAATGGGAAAAGTG 754

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RESULT 4
US-09-614-221A-451/c
; Sequence 451, Application US/09614221A
; Patent No. 6723837
; GENERAL INFORMATION:
; APPLICANT: Karunanandaa, Balasubramanian
; APPLICANT: Yu, Jaehyuk
; APPLICANT: Kishore, Ganesh M.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED
; FILE REFERENCE: 16516.075
; CURRENT APPLICATION NUMBER: US/09/614, 221A
; PRIOR FILING DATE: 2000-07-12
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 626

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; SEQ ID NO 451
; LENGTH: 612
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-614-221A-451

Alignment Scores:
Pred. No.: 4.76e-06 Length: 612
Score: 132.50 Matches: 61
Percent Similarity: 41.35% Conservative: 25
Best Local Similarity: 29.33% Mismatches: 73
Query Match: 12.68% Indels: 49
DB: 4 Gaps: 9

US-09-980-758A-8 (1-209) x US-09-614-221A-451 (1-612)

QY 7 AsnProArgGluLysLysMetSerGluArgLysArgGluLeuAlaGluAlaSerSer 26
Db 557 AACAGAAGAGAGTTAAGGCTTCCAAACCAAGCAAGAA---GAAAAGCTAAGGCC 504
QY 27 ThrSerPheSerProLeuLysLysThrLysLeuAsnAspSerSerAspSerProAsp 46
Db 503 GTCTCTTCTCT---TCCTCCGAATCTTCATCTCA 471
QY 47 SerHisAspValIleValPheAlaValSerSerSerValAlaSerSerAlaLeu 66
Db 470 TCT---TCATCTTCAATCTGAATCTGAATCTGAATCTTCATCTTCATCTCA 471
QY 67 AlaSerAspGluCysSerValThrIleGlyGlyGluLysArgGlnSerSerSerIle 86
Db 434 TCTGAATCTGAATCTTCATCTTCATCTTCATCTTCATCTTCATCTTCATCTTC 375
QY 87 SerSerGlyCysPheThrSerGluSer-----LysGluLeuAlaLysAsn 101
Db 374 TCTTCT-----GACAGCGAAAGTGAAGCTGAAACCAAGCAAGCAAGCAAGCA 324
QY 102 SerSerSerPheGlyValAsp---LeuGluAspHisGlnIleGluThrGluThr 120
Db 323 TCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 264
QY 121 SerThrPheIleThrSerAsnPheArgLysGluThrSerProValSerGluGly 140
Db 263 ACCAAGAGGAGAGTCAAAAGAAATCTTCTAGCTCTGATTCATCTTCATCTTCAT 204
QY 141 GluThrThrThrGluMetGluSerSerSerSerAlaThrLysArgLysGlnProGlyValArg 160
Db 203 GATAGCGAAAGCGAAAGGAGAGTCTAACGATAAGAAACGTAATAATCT----- 156
QY 161 LysThrProThrAlaAlaGluIleGluAspLeuPheSerGluLeuGluSerProAsp 180
Db 155 -----GAGGACGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
QY 181 LysLysLysGlnPheIleGluLysTyAsnPheAspIleValAsnAspGluPro----- 198
Db 119 AACAGAAGCAAAAGAAATGAAGAA-----ACCAAGAACCAAGCAAGTACT 78
QY 199 ---LeuGluGlyArgTyLysTrp 205
Db 77 ATTTTCGTTGGTAGACTATCGTGG 54

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RESULT 5
US-07-667-276A-3
; Sequence 3, Application US/07667276A
; Patent No. 5470971
; GENERAL INFORMATION:
; APPLICANT: Kondo, Keiji
; APPLICANT: Inouye, Masayori
; TITLE OF INVENTION: STRESS-INDUCED PROTEINS, GENES CODING
; TITLE OF INVENTION: THEREFOR, TRANSFORMED CELLS OF ORGANISMS, METHODS AND
; TITLE OF INVENTION: APPLICATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weiser & Associates

```

STREET: 230 S. Fifteenth Street, Suite 500  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19102

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT AFFIDAVIT DATA:  
APPLICATION NUMBER: US/07/667,276A

FILING DATE: 11-MAR-1991

CLASSIFICATION: 435

**ATTORNEY/AGENT INFORMATION:**

NAME: Weiser, Gerard J.

REGISTRATION NUMBER: 19,763

REFERENCE/DOCKET NUMBER: 377.5351P

TELECOMMUNICATION INFORMATION

TELEPHONE: 215-875-8383

TELEFAX: 215-875-8394

INFORMATION FOR SEQ ID NO: 3:

### SEQUENCE CHARACTERISTICS:

LENGTH: 2017 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: unknown

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: internal

ORIGINAL SOURCE:

**ORGANISM:** *Saccharomyces cerevisiae*

STRAIN: S288C

**FEATURE:**

NAME/KEY: CD

LOCATION: 484..1725

**FEATURE:**

NAME/KEY: misc\_feature

LOCATION: 1

OTHER INFORMATION: /note= "Base #1 of Sequence No. 5470971 3

OTHER INFORMATION: corresponds to base -483 of the sequence listed in

OTHER INFORMATION: Figure 11 of the application"

1-667-276A-3

Alignment Scores:		2.97e-05	Length:	2017
Pred. No.:	Score:	132.50	Matches:	61
	Percent Similarity:	41.35%	Conservative:	25
	Best Local Similarity:	29.33%	Mismatches:	73
	Query Match:	12.68%	Indels:	49
DB:		1	Gaps:	9

US-09-980-758A-8 (1-209) x US-07-667-276A-3 (1-2017)

**Qy**      7    AsnProArgGluLysLysMetSerClnArgLysArgGluLeuAlaGluGluAlaSerSer    26  
|||    :    :    :    :    |||    :    :    :    :    :    :    :    :    :    :    :    :  
**Db**     511   AACAAAGAGGAAGTTAAGGTTCCAAACCAAGCCCAAGAA-----GAAAAGCTAAGGCC    564

**Qy**      27 ThrSerPheSerProLeuLysLysThrLysLeuAsnAspSerSerAspSerSerProAsp 46  
          |||     |||       |       |       |       |       |       |  
**Db**      565 GTCCTTCTCT-----TCTCCGAATCTTCATCTCA 597

Db  
598 TCT-----TCATCTTCATCTGAATCTGAATCTGAGCTGAG 633

Ov 67 AlaserAspGluCvsserValThrIleGlvGlvGlvUserAspGlnSerSerSeriLe 86

634 TCTGAACTCTGATCTCTTCATCTCTCATCTCTGATCTTGAATCTCTCTCTCTTCATCG 693

Qy 87 SerSerGlyCysPheThrSerGluSer-----LysGluIleAlaLysAsn 101

## RESULT 8

; CURREN

TYPE ;

**Db**

ov

Qy

```

Db 190 AGTACATCGGTAAAGTGAATCATCAAGTACAGCGTTTCAGATTCA-----ACAAAGT 140
Qy 162 ThrProThrAlaAlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAsp 180
Db 139 ACATCGACATCAAGAAAGTGCATCAACGTCACAGCGAGTGAATCAACAAAGTGAA 83

RESULT 9
US-09-134-001C-1685/c
; Sequence 1685, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1685
; LENGTH: 3561
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1685

Alignment Scores:
Pred. No.: 0.00154 Length: 3561
Score: 121.00 Matches: 51
Percent Similarity: 41.21% Conservative: 31
Best Local Similarity: 25.63% Mismatches: 87
Query Match: 11.58% Indels: 30
DB: 3 Gaps: 4

US-09-980-758A-8 (1-209) x US-09-134-001C-1685 (1-3561)
Qy 9 ArgGluLysLysMetSerGluArgLysGluLeuAlaGluLysLys 25
Db 677 AGAGAGAGTGAATCAACAAAGTCCAAAGTCAAGTACGTCAATTGAGTGAATCAACAAAGCGTTT 618

Qy 26 -----SerThrSerPheSerProLeuLysLysThrLysLysLeuAsnAsp 39
Db 617 TCAGATTCAACAAAGTACATCGACATCCGACATCGCTCAACCTCAACAAAGTCAGAGTGAC 558

Qy 40 SerSerAspSerSerProAspSerHisAspValIleValPheAlaValSerSerSer 59
Db 557 TCAACAAAGTGAAGTACATCGTTAAAGTGAAGTCGACAAAGCACAAGCGTTTCAGATTCAACA 498

Qy 60 ValAlaSerSerAlaAlaLeuAlaSerAspGluCysSerVal----- 73
Db 497 AGCGGTCAACGTCAAGTCAAGTGCATCAACATCAACGAGCGTGAGTGACTCCAAATAGCGCA 438

Qy 74 -----ThrIleGlyGlyGluGluSerAspGlnSerSer 84
Db 437 AGTACGTCAATTAAAGTGGCTCAACAAAGTCAACAGCGTTTCAGACTCAACGAGTACGTGACA 378

Qy 85 SerIleSerSerGlyCysPheThrSerGluSerLysGluIleAlaLysAsnSerSer--- 103
Db 377 TCAGCAAGTGCATCAACATCAACGAGCGAGCGAGCTCCGATAGCGCAAGTACGTGTTA 318

Qy 104 -----SerPheGlyValAspLeuGluAspHisGlnIleGluThrGluThrSer 121
Db 317 AGTGGCTCAACAAAGTCAACAGCATTTTCAGACTCAACGAGTACGTCCACATCAACAGAGTGGC 258

Qy 122 ThrPheIleThrSerAsnPheArgLysGluThrSerProValSerGluGlyLeuGlu 141
Db 257 TCCACATCCATCAACAAAGTGCATCCACATCAACGAGTGTGAGTGAGTCAGACAGTGAA 198

Qy 142 ThrThrThrGluMetGluSerSerAlaThrLysArgLysGlnProGlyValArgLys 161
Db -----

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Db 197 AGTACATCGGTAAAGTGAATCATCAAGTACAGCGTTTCAGATTCA-----ACAAAGT 147
Qy 162 ThrProThrAlaAlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAsp 180
Db 146 ACATCGACATCAAGAAAGTGCATCAACGTCACAGCGAGTGAATCAACAAAGTGAA 90

RESULT 10
US-09-214-564A-5/c
; Sequence 5, Application US/09214564A
; Patent No. 6150515
; GENERAL INFORMATION:
; APPLICANT: Sharp, Phillip A.
; APPLICANT: Zhou, Qiang
; TITLE OF INVENTION: TAT-SF: Cofactor For Stimulation Of Transcriptional
; FILE REFERENCE: M0656/7042
; CURRENT APPLICATION NUMBER: US/09/214,564A
; CURRENT FILING DATE: 1999-08-18
; PRIOR APPLICATION NUMBER: US 60/021,218
; PRIOR FILING DATE: 1996-07-03
; PRIOR APPLICATION NUMBER: US 60/033,152
; PRIOR FILING DATE: 1996-12-13
; PRIOR APPLICATION NUMBER: PCT/US97/11713
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 2672
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 58..2319
US-09-214-564A-5

Alignment Scores:
Pred. No.: 0.00252 Length: 2672
Score: 117.50 Matches: 53
Percent Similarity: 44.50% Conservative: 32
Best Local Similarity: 27.75% Mismatches: 85
Query Match: 11.24% Indels: 21
DB: 3 Gaps: 6

US-09-980-758A-8 (1-209) x US-09-214-564A-5 (1-2672)
Qy 4 LeuProLysAsnProArgGluLysLysMetSerGluArgLysArgGluLeuAlaGluGlu 23
Db 2449 CTCCTCAAAACCCACCAAGTCCCTCTCATCAGATCGTCAACAACTTCTACTGGAA 2190

Qy 24 AlaSerSerThrSer-----PheSerProLeuLysLysThrLysLeuAsnAspSerSer 41
Db 2189 TCTTCTCTCTCATCAACAACTTCTCA--TTGGAATCATCATCTTCGACAACTTTTCG 2133

Qy 42 AspSerSerProAspSerHisAspValIleValPheAlaValSerSerSerValAla 61
Db 2132 TCAGATCTTCAACTTCTCTTTCCA-----TCTGCATCTTCTATCTCTTGTGCA 2085

Qy 62 SerSerAlaAla-----LeuAlaSerAspGluCysSerValThrIleGlyGlyGlu 78
Db 2084 TCTGACTCTTCAACAGCTTTTTCATCTGCATCACCCTTCTCCGCTTTTATCAGCAGCT 2025

Qy 79 GluSerAspGlnSerSerSerIleSerSerGlyCysPheThrSerGluSerLys----- 96
Db 2024 TCAAGCCCTTTTTCATCTGCATATCTTCACTCTTCTCATCAGACTCATCAAAAT 1965

Qy 97 -----GluIleAlaLysAsnSerSerPheGlyValAspLeuGluAspHisGlnIle 114
Db 1964 ACTTTTTCATATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC 1905

Qy 115 GluThrGluThrGluThrSerThrPhe-----IleThrSerAsnPheArgLysGlu 131
Db 1904 TCAGAGCTTCTCTCATCTAACACATTTTTCAGAGCGGTCACTTCAATTCGAGTTTCA 1845

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QY 132 ThrSerProValSerGluGlyLeuGlyGluThr-----ThrThrGluMetGluSer 148
Db 1844 GAGTCATTTCTTCAACTCTTTGTCAAGAACATTTTCAGAGCTCCCTTTTCAGAACCT 1785
QY 149 SerSerAlaThrLysArgLysGlnProGlyValArgLysThrProThrAlaAlaGluIle 168
Db 1784 TCTCGTCCAAATCTTTTCGAGACCA---TTTCTTCAAATCTCTTTTCGGAGCCATCT 1728
QY 169 GluAspLeuPheSerGluLeuGluSerProAsp 179
Db 1727 TCAGACTGTTTTTCAGAGCAGTCTTCATCAGAC 1695

RESULT 11
US-09-214-564A-1/c
; Sequence 1, Application US/09214564A
; Patent No. 6150515
; GENERAL INFORMATION:
; APPLICANT: Sharp, Phillip A.
; APPLICANT: Zhou, Qiang
; TITLE OF INVENTION: TAT-SF: Cofactor For Stimulation Of Transcriptional
; FILE REFERENCE: M0656/7042
; CURRENT FILING DATE: 1999-08-18
; PRIOR FILING DATE: 1996-07-03
; PRIOR APPLICATION NUMBER: US 60/021,218
; PRIOR FILING DATE: 1996-07-03
; PRIOR APPLICATION NUMBER: US 60/033,152
; PRIOR FILING DATE: 1996-12-13
; PRIOR APPLICATION NUMBER: PCT/US97/11713
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2815
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 110..2371
; NAME/KEY: unsure
; LOCATION: 46..46
; OTHER INFORMATION: n = a, c, g or t
; NAME/KEY: unsure
; LOCATION: 2731..2731
; OTHER INFORMATION: n = a, c, g or t
US-09-214-564A-1

Alignment Scores:
Pred. No.: 0.00273 Length: 2815
Score: 117.50 Matches: 53
Percent Similarity: 44.50% Conservative: 32
Best Local Similarity: 27.75% Mismatches: 85
Query Match: 11.24% Indels: 21
DB: 3 Gaps: 8

US-09-980-758A-8 (1-209) x US-09-214-564A-1 (1-2815)
QY 4 LeuProLysAsnProArgGluLysLysMetSerGluArgLysArgGluLeuAlaGluGlu 23
Db 2301 CTCCTCAAAACCCCAAGTCCCTCTCATCAGAACTGTCACAACTTCTCACTGGAA 2242
QY 24 AlaSerSerThrSer-----PheSerProLeuLysLysThrLysLeuAsnAspSerSer 41
Db 2241 TCTTCTCTCTCATCAACAACTTCTCA---TTGGAATCATCATCTTCGAACAACTTTTCG 2185
QY 42 AspSerSerProAspSerHisAspValIleValPheAlaValSerSerSerValAla 61
Db 2184 TCAGCATCTCAACTCTCTTTTCCA-----TCTGCATCTTCATCTTCTTGTGCA 2137
QY 62 SerSerAlaAla-----LeuAlaSerAspGluCysSerValThrIleGlyGlu 78
Db 2136 TCTGACTCTTCAACAGCTTTTCACTCTGCATCACCTTCTTCGCCCTTTTATCAGCAGCT 2077
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QY 79 GluSerAspGlnSerSerSerSerGlyCysPheThrSerGluSerLys----- 96
Db 2076 TCAAGCCCTTTTCATCTGTCATATTCTCTCTTCATCAGACTCATCATCAAT 2017
QY 97 -----GluIleAlaLysAsnSerSerPheGlyValAspLeuGluAspHisGluIle 114
Db 2016 ACTTTTTCATATGATCTCTCTCTCTCTTTTCATCTGAATCTTCGTCAAACTCTCTC 1957
QY 115 GluThrGluThrGluThrSerThrPhe-----IleThrSerAsnPheArgLysGlu 131
Db 1956 TCAGAGCCTTCTCATCTAACTTTTTCAGAGCCGTCATCTTCAAATTCGGAGTTTCA 1897
QY 132 ThrSerProValSerGluGlyLeuGluThr-----ThrThrGluMetGluSer 148
Db 1896 GAGTCATTTTCTTCAACTCTTTTCAGAGCAGTCTTCATCAGAC 1747
QY 149 SerSerAlaThrLysArgLysGlnProGlyValArgLysThrProThrAlaAlaGluIle 168
Db 1836 TCTCGTCCAAATCTTTTCGAGACCA---TTTCTTCAAATCTCTTTTCGGAGCCATCT 1780
QY 169 GluAspLeuPheSerGluLeuGluSerProAsp 179
Db 1779 TCAGACTGTTTTTCAGAGCAGTCTTCATCAGAC 1747

RESULT 12
US-09-902-540-1016/c
; Sequence 1016, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1016
; LENGTH: 11805
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(11805)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1016

Alignment Scores:
Pred. No.: 0.0282 Length: 11805
Score: 117.00 Matches: 55
Percent Similarity: 41.53% Conservative: 21
Best Local Similarity: 30.05% Mismatches: 82
Query Match: 11.20% Indels: 26
DB: 4 Gaps: 5

US-09-980-758A-8 (1-209) x US-09-902-540-1016 (1-11805)
QY 5 ProLysAsnProArgGluLysLysMetSerGluArgLysArgGluLeuAlaGluAla 24
Db 8324 CCGAGTCGTCTCC--GAATCTCTCTCCGCGCATCTCATCGAGCGCATCTTCCGAG 8266
QY 25 SerSerThrSerPheSerProLeuLysLysThrLysLeuAsnAspSerSerSer 44
Db 8265 TCTCATCGAGCATCTCTCGCATCTTCATCGAGCATCTCTTCCGAGTCTCTCTC 8206
QY 45 ProAspSerHisAspValIleValPheAlaValSerSerSerValAlaSerSerAla 64
Db 8205 GACGACTCTCGGAATCTCTCATCTCGGCTCGTCAGACTCTCTCGTCATCGAGTCTCG 8146
QY 65 AlaLeuAlaSerAspGluCysSerValThrIleGlyGluGluSerAspGlnSerSer 84
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Db 8145 GATTTCATCATCTCGCGCTGCTCAGACCTCTCTGTCATCGGAGTCGTGGATTTCATCATCG 8086  
Qy 85 SerIleSerSerGlyCysPheThrSerGluSerLysGluIleAlaLysAsnSerSerSer 104  
Db 8085 TCGCGCTGCTCAGACTCTCATCTCGGAGTCGTGGAGTCATCATCTCGCGCTGCT 8026  
Qy 105 PheGlyValAspLeuGluAspHisGlnIleGluThrGluThrSerThrPheIle 124  
Db 8025 -----GATTGCGCGCCAGCCCTCCGAGCGCAGCAGGATGCTCGACCTCCGCG 7975  
Qy 125 ---ThrSerAsnPheArgLysGluThrSer 133  
Db 7974 AGAATCTCTGCTTCGCGCGAGCACCAGCTCAGTGAATTCACCTGCGCCACGGACAAT 7915  
Qy 134 -----ProValSerGluGlyLeuGlyThrThr 151  
Db 7914 GGCACCGAGGTGACCCAGGA---GGTTCCGTCGCGGCTCTCTCGTCGCGTCGCGCC 7858  
Qy 152 ThrLys-ArgLysGlnProGly-----ValArgLysThrProTh 164  
Db 7857 GAGAGGGCGCCACACCGGGGCGAGCCGTATCCGCCACCACTGCCACCGGACACCGAC 7798  
Qy 164 rAlaAla 166  
Db 7797 TCCTGCG 7791

## RESULT 13

US-09-270-767-1642  
; Sequence 1642, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1642  
; LENGTH: 938  
; TYPE: DNA  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-1642

Alignment Scores:  
Pred. No.: 0.000661 Length: 938  
Score: 116.50 Matches: 49  
Percent Similarity: 37.85% Conservative: 32  
Best Local Similarity: 22.90% Mismatches: 94  
Query Match: 11.15% Indels: 39  
DB: 4 Gaps: 6

US-09-980-758A-8 (1-209) x US-09-270-767-1642 (1-938)

Qy 20 LeuAlaGluAlaSerSerThrSerPheSerProLeuLysLysThrLysLeuAsnAsp 39  
Db 16 CTGTCCAGTGATGGATCAACCAAGATCACTGATGCTTCTTAATGCTCTACTGAGGCG 75  
Qy 40 SerSerAspSerSerProAsp----- 46  
Db 76 ACCACTGATGGCTCAACTGATGAATCACTGATGGTTCTCTTAATGCTCTACTGAGGCG 135  
Qy 47 -----SerHisPheValIleValPheAlaValSerSerSerValAla 61  
Db 136 TCTACTGAAGCGCGAAGCGAGGACACCAATCTCCACGGAGTCTCCGGATCAACCGAA 195  
Qy 62 SerSerAlaAlaLeuAlaSerAspGluCysSerValThrIleGlyGlyGluSerAsp 81  
Db 196 AGCACCAGCGCCATCGCCAGTATGGT---TCGACCAAGGAGGAGTACCGTCGAGGAC 252  
Qy 82 GlnSerSerSerIleSerSerGlyCysPhe-----ThrSerGlu 94  
Db 82 GlnSerSerSerIleSerSerGlyCysPhe-----ThrSerGlu 94

Db 253 CTGTCCAGTTCACCAAGCTCTGATGTATCTGATTCTTACCATCACGAGCTCTCACCT 312  
Qy 95 SerLysGluIleAla---LysAsnSerSerSerPheGlyValAspLeuGluAspHisGln 113  
Db 313 TCCACTGAGTATCTGGTTCACAGACTCATCTCTTCCACAGATGGTTCCTCAACAGAT 372  
Qy 114 IleGluThrGluThrGluThrSerThrPheIleThrSerAsnPheArgLysGluThrSer 133  
Db 373 GCTTCTCCACTGAGGCTCTCTTACCAGATGTCTAGTAATCT-----ACAGATAGT 423  
Qy 134 ProValSerGluGlyLeuGlyGluThr-----ThrThr 144  
Db 424 ACTGTTAGTGGAGTACACGACACTACCGAAAGCGGTCCACGAGGAAAGTACTACC 483  
Qy 145 GluMetGluSerSerAlaThrLysArgLysGlnProGlyValArgLysThrProThr 164  
Db 484 GAAGCTTCCACTGAAGACACACCGAAGGATCCACACAGCACCACCGATCTG 543  
Qy 165 AlaAlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAspLysLysGln 184  
Db 544 GACAGCACCACTGATATCTGGAGCACCACTGATAAGGATGACGAATCGGAGCAGT 603  
Qy 185 PheIleGluLysTyrAsnPheAspIleValAsnAspGluPro 198  
Db 604 ACTCCTTACTCTTTGATCTGAAAGTTACCAAGAGCAAGCCC 645

## RESULT 14

US-09-270-767-16924  
; Sequence 16924, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16924  
; LENGTH: 938  
; TYPE: DNA  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-16924

Alignment Scores:  
Pred. No.: 0.000661 Length: 938  
Score: 116.50 Matches: 49  
Percent Similarity: 37.85% Conservative: 32  
Best Local Similarity: 22.90% Mismatches: 94  
Query Match: 11.15% Indels: 39  
DB: 4 Gaps: 6

US-09-980-758A-8 (1-209) x US-09-270-767-16924 (1-938)

Qy 20 LeuAlaGluAlaSerSerThrSerPheSerProLeuLysLysThrLysLeuAsnAsp 39  
Db 16 CTGTCCAGTGATGGATCAACCAAGATCACTGATGCTTCTTACACACACTGACATC 75  
Qy 40 SerSerAspSerSerProAsp----- 46  
Db 76 ACCACTGATGGCTCAACTGATGAATCACTGATGGTTCTCTTAATGCTCTACTGAGGCG 135  
Qy 47 -----SerHisPheValIleValPheAlaValSerSerSerValAla 61  
Db 136 TCTACTGAAGCGCGAAGCGAGGACACCAATCTCCACGGAGTCTCCGGATCAACCGAA 195  
Qy 62 SerSerAlaAlaLeuAlaSerAspGluCysSerValThrIleGlyGlyGluSerAsp 81  
Db 196 AGCACCAGCGCCATCGCCAGTATGGT---TCGACCAAGGAGGAGTACCGTCGAGGAC 252  
Qy 82 GlnSerSerSerIleSerSerGlyCysPhe-----ThrSerGlu 94  
Db 253 CTGTCCAGTTCACCAAGCTCTGATGTATCTGATTCTTACCATCACGAGCTCTCACCT 312

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QY 95 SerLysGluIleAla---LysAsnSerSerSerPheGlyValAspLeuGluAspHisGln 113
Db 313 TCACAGTAAATCTCGTTCACAGACTCATCTCTCCACAGATGGTTCCTCAACAGAT 372
QY 114 IleGluThrGluThrGluThrSerPheIleThrSerAsnPheArgLysGluThrSer 133
Db 373 GCTTCTCCACTGAGGCTTCCTACCGATGTCACATGATCT-----ACAGATAGT 423
QY 134 ProValSerGluGlyLeuGlyGluThr-----ThrThr 144
Db 424 ACTGTTAGTGGAGGTACACGAGACACTACGAAAGCGGTCCAAACGAGGAGAAAGTACTACC 483
QY 145 GluMetGluSerSerSerAlaThrLysArgLysGlnProGlyValArgLysThrProThr 164
Db 484 GAAGGCTCCACTGAAAGCAACCGAAGGATCCACAGACAGCACCCCAATCCACCGATCTG 543
QY 165 AlaAlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAspLysLysLysGln 184
Db 544 GACAGCACCAACGATGATATCGGACACCAAGTAAAGATGACGAATCGGAGACGACT 603
QY 185 PheIleGluLysTyraAsnPheAspIleValAsnAspGluPro 198
Db 604 ACTCTTACTCTCTTGATTCGAAGTTACCAAGACGAGCC 645

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# RESULT 15

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US-09-949-016-16775
; Sequence 16775, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16775
; LENGTH: 12695
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16775

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Alignment Scores:

Pred. No.:	Score:	Length:	Matches:
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43.33%	Conservative:	25	
26.67%	Mismatches:	5	
11.15%	Indels:	1	
4	Gaps:		

US-09-980-758A-8 (1-209) x US-09-949-016-16775 (1-12695)

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QY 2 ArgAspLeuProLysAsnProArgGluLysLysMetSerGluArgLysArgGluLeuAla 21
Db 9274 AAGGACAACTAAACAACACTCTCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCC 9333
QY 22 GluGluAlaSerSerPheSerProLeuLysLysThrLysLeuAsnAspSerSer 41
Db 9334 TCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 9393
QY 42 AspSerSerProAspSerHisAspValIleValPheAlaValSerSerSerValAla 61
Db 9394 TCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 9438
QY 62 SerSerAlaAlaLeuAlaSerAspGluCysSerValThrIleGlyGlyGluSerAsp 81

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Db 9439 TCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCC 9498
QY 82 GlnSerSerSerIleSerSerGlyCysPheThrSerGluSerLysGluIleAlaLysAsn 101
Db 9499 TCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCC 9558
QY 102 SerSerSerPheGlyValAspLeuGluAspHisGlnIleGluThrGluThrGluThrSer 121
Db 9559 TCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCC 9618
QY 122 ThrPheIleThrSerAsnPheArgLysGluThrSerProValSerGluGlyLeuGlyGlu 141
Db 9619 TCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCC 9678
QY 142 ThrThrThrGluMetGluSerSerAla 151
Db 9679 TCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCC 9708

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 30, 2005, 11:43:39 ; Search time 656 Seconds  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1007	96.4	824	18 US-10-451-139-7	Sequence 7, Appli
3	351.5	33.6	642	9 US-09-733-507-8	Sequence 8, Appli
4	351.5	33.6	642	18 US-10-451-139-8	Sequence 8, Appli
5	213.5	20.4	1040	18 US-10-424-599-69339	Sequence 69339, A
6	181	17.3	904	9 US-09-733-507-1	Sequence 1, Appli
7	181	17.3	905	18 US-10-451-139-1	Sequence 1, Appli
8	177	16.9	861	18 US-10-451-139-18	Sequence 18, Appli
9	177	16.9	932	18 US-10-688-291-1	Sequence 1, Appli
10	174.5	16.7	1261	18 US-10-424-599-67348	Sequence 67348, A
11	174	16.7	660	9 US-09-733-507-3	Sequence 3, Appli
12	174	16.7	660	18 US-10-451-139-3	Sequence 3, Appli
13	172	16.5	1237	18 US-10-424-599-40086	Sequence 40086, A
14	168.5	16.1	804	9 US-09-733-507-15	Sequence 15, Appli
15	168.5	16.1	804	18 US-10-451-139-14	Sequence 14, Appli
16	162.5	15.6	1290	18 US-10-451-139-16	Sequence 16, Appli
17	159	15.2	755	9 US-09-733-507-6	Sequence 6, Appli
18	159	15.2	755	18 US-10-451-139-6	Sequence 6, Appli
19	155	14.8	797	18 US-10-451-139-20	Sequence 20, Appli
20	153.5	14.7	654	21 US-10-890-629-3	Sequence 3, Appli
21	153.5	14.7	1110	18 US-10-425-114-21130	Sequence 21130, A
22	153.5	14.7	1110	20 US-10-425-115-69492	Sequence 69492, A
23	153	14.6	875	18 US-10-688-291-3	Sequence 3, Appli
24	153	14.6	1242	17 US-10-333-006-9	Sequence 9, Appli
25	153	14.6	1671	19 US-10-437-963-18387	Sequence 92632, A
26	151	14.4	906	19 US-10-437-963-18387	Sequence 18387, A
27	151	14.4	1067	17 US-10-333-006-43	Sequence 43, Appli
28	150.5	14.4	533	9 US-09-733-507-9	Sequence 9, Appli
29	150.5	14.4	533	18 US-10-451-139-9	Sequence 9, Appli
30	148.5	14.2	1022	9 US-09-770-443-210	Sequence 210, App
31	148	14.2	642	21 US-10-890-629-1	Sequence 1, Appli
32	148	14.2	1112	18 US-10-425-114-25318	Sequence 25318, A
33	148	14.2	1122	20 US-10-425-115-83466	Sequence 83466, A
34	144	13.8	443	9 US-09-733-507-4	Sequence 4, Appli
35	144	13.8	443	18 US-10-451-139-5	Sequence 5, Appli
36	142	13.6	1360	18 US-10-424-599-92958	Sequence 92958, A
37	139	13.3	377	9 US-09-733-507-5	Sequence 5, Appli
38	139	13.3	377	18 US-10-451-139-4	Sequence 4, Appli
39	138.5	13.3	1183	19 US-10-437-963-96091	Sequence 96091, A
40	138.5	13.3	1721	19 US-10-451-467A-261	Sequence 261, App
41	136.5	13.1	1193	18 US-10-688-291-5	Sequence 5, Appli
42	135.5	13.0	602	19 US-10-767-701-4699	Sequence 4699, Ap
43	134	12.8	765	21 US-10-890-629-11	Sequence 11, Appli
44	134	12.8	1372	9 US-09-993-308-1	Sequence 1, Appli
45	134	12.8	1372	11 US-09-993-808B-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-733-507-7  
; Sequence 7, Application US/09733507  
; Patent No. US20010025379A1  
; GENERAL INFORMATION:  
; APPLICANT: Agriculture and Agri-Food Canada; The University of Saskatchewan  
; TITLE OF INVENTION: Cyclin Dependant Kinase Inhibitors as Plant Growth  
; TITLE OF INVENTION: Regulators  
; FILE REFERENCE: 81601-3  
; CURRENT APPLICATION NUMBER: US/09/733,507  
; PRIOR FILING DATE: 2000-12-02  
; PRIOR APPLICATION NUMBER: CA 2,256,121  
; PRIOR FILING DATE: 1998-12-31  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7

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; LENGTH: 824
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-733-507-7

Alignment Scores:
Pred. No.: 2,75e-102 Length: 824
Score: 1007.00 Matches: 202
Percent Similarity: 99.51% Conservative: 0
Best Local Similarity: 99.51% Mismatches: 1
Query Match: 96.36% Indels: 0
DB: 9 Gaps: 0

US-09-980-758A-8 (1-209) x US-09-733-507-7 (1-824)
Qy 6 LysAenProArgGluLysMetSerGluArgLysArgGluLeuAlaGluAlaSer 25
Db 28 AAAAAATCCAGAGAGAAAAAATGAGCGAGAGAAAGCGAGAGCTTGCAGAAAGAGCTTCA 87
Qy 26 SerThrSerPheSerProLeuLysLysThrLysLeuAsnAspSerSerAspSerPro 45
Db 88 AGCACAGCTTCTCACCAGTGAAGAAACGAGCTTAATGATTCTTCTGATTCATCACCG 147
Qy 46 AspSerHisAspValIleValPheAlaValSerSerSerValAlaSerSerAlaAla 65
Db 148 GACTCTCATGCTCATCGTCTTCGCGGTTTCATCTTCTTCGTTGCTTCGCGCGGCT 207
Qy 66 LeuAlaSerAspGluCysSerValThrIleGlyGlyGluGluSerAspGlnSerSer 85
Db 208 TTAGCGTCTGATGAATGTTCCGTTACCATCGGTGAGAGAAAGTGATCGTCTCGAGT 267
Qy 86 IleSerSerGlyCysPheThrSerGluSerLysGluIleAlaLysAsnSerSerPhe 105
Db 268 ATCAGCTCCGGTTGTTTCCACGAGTGAATCGAAAGAAATCGCGAAACAGTTCGTCGTT 327
Qy 106 GlyValAspLeuGluAspHisGlnIleGluThrGluThrGluThrSerThrPheIleThr 125
Db 328 GGTGTAGATCTGGAGGATCATCAAAATCGAAACCGAAACCGAAACCTCAACATTCATCACC 387
Qy 126 SerAenPheArgLysGluThrSerProValSerGluLysGlyLeuGluThrThrGlu 145
Db 388 AGCAATTTTCAGAAAAGACGAGTCCAGTGTAGTGGGGTTGGGAGAAACGACACAGAA 447
Qy 146 MetGluSerSerAlaThrLysArgLysGlnProGlyValArgLysThrProThrAla 165
Db 448 ATGGAATCATCATCGCAACGAGAGAAACACACCGGGGGTTCAGAGACATCCAAACGGGG 507
Qy 166 AlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAspLysLysGlnPhe 185
Db 508 GCGGAGATTGAGGATTTGTTCTCGAGCTAGAGAGTCAAGACGATTAAGAAGCAATTC 567
Qy 186 IleGluLysTyrAsnPheAspIleValAsnAspGluProLeuGluGlyArgTyrIleYsrp 205
Db 568 ATAGAAAAGTACAACTTCGATATTGTCAATGACGAACCGCTTGAAGGTCGCTACAAAGTGG 627
Qy 206 AspArgLeu 208
Db 628 GATCGACTT 636

RESULT 2
US-10-451-139-7
; Sequence 7, Application US/10451139
; Publication No. US20040098763A1
; GENERAL INFORMATION:
; APPLICANT: WANG, HONG
; APPLICANT: ZHOU, YONGMING
; APPLICANT: FOWKE, LARRY C.
; APPLICANT: HER MAJESTY IN RIGHT OF CANADA AS REPRESENTED BY THE MINISTER OF
; APPLICANT: AGRICULTURE AND AGRI-FOOD CANADA
; TITLE OF INVENTION: MODULATION OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR
; TITLE OF INVENTION: ACTIVITY
; FILE REFERENCE: 4810-62237
; CURRENT APPLICATION NUMBER: US/10/451,139
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; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: WO PCT/CA01/01825
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,908
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 7
; LENGTH: 824
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-451-139-7

Alignment Scores:
Pred. No.: 2,75e-102 Length: 824
Score: 1007.00 Matches: 202
Percent Similarity: 99.51% Conservative: 0
Best Local Similarity: 99.51% Mismatches: 1
Query Match: 96.36% Indels: 0
DB: 18 Gaps: 0

US-09-980-758A-8 (1-209) x US-10-451-139-7 (1-824)
Qy 6 LysAenProArgGluLysLysMetSerGluArgLysArgGluLeuAlaGluAlaSer 25
Db 28 AAAAAATCCAGAGAGAAAAAATGAGCGAGAGAAAGCGAGAGCTTGCAGAAAGAGCTTCA 87
Qy 26 SerThrSerPheSerProLeuLysLysThrLysLeuAsnAspSerSerAspSerPro 45
Db 88 AGCACAGCTTCTCACCAGTGAAGAAACGAGCTTAATGATTCTTCTGATTCATCACCG 147
Qy 46 AspSerHisAspValIleValPheAlaValSerSerSerValAlaSerSerAlaAla 65
Db 148 GACTCTCATGCTCATCGTCTTCGCGGTTTCATCTTCTTCGTTGCTTCGCGCGGCT 207
Qy 66 LeuAlaSerAspGluCysSerValThrIleGlyGlyGluGluSerAspGlnSerSer 85
Db 208 TTAGCGTCTGATGAATGTTCCGTTACCATCGGTGAGAGAAAGTGATCGTCTCGAGT 267
Qy 86 IleSerSerGlyCysPheThrSerGluSerLysGluIleAlaLysAsnSerSerPhe 105
Db 268 ATCAGCTCCGGTTGTTTCCACGAGTGAATCGAAAGAAATCGCGAAACAGTTCGTCGTT 327
Qy 106 GlyValAspLeuGluAspHisGlnIleGluThrGluThrGluThrSerThrPheIleThr 125
Db 328 GGTGTAGATCTGGAGGATCATCAAAATCGAAACCGAAACCGAAACCTCAACATTCATCACC 387
Qy 126 SerAenPheArgLysGluThrSerProValSerGluLysGlyLeuGluThrThrGlu 145
Db 388 AGCAATTTTCAGAAAAGACGAGTCCAGTGTAGTGGGGTTGGGAGAAACGACACAGAA 447
Qy 146 MetGluSerSerAlaThrLysArgLysGlnProGlyValArgLysThrProThrAla 165
Db 448 ATGGAATCATCATCGCAACGAGAGAAACACACCGGGGGTTCAGAGACATCCAAACGGGG 507
Qy 166 AlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAspLysLysGlnPhe 185
Db 508 GCGGAGATTGAGGATTTGTTCTCGAGCTAGAGAGTCAAGACGATTAAGAAGCAATTC 567
Qy 186 IleGluLysTyrAsnPheAspIleValAsnAspGluProLeuGluGlyArgTyrIleYsrp 205
Db 568 ATAGAAAAGTACAACTTCGATATTGTCAATGACGAACCGCTTGAAGGTCGCTACAAAGTGG 627
Qy 206 AspArgLeu 208
Db 628 GATCGACTT 636

RESULT 3
US-09-733-507-8
; Sequence 8, Application US/09733507
; Patent No. US20010025379A1
; GENERAL INFORMATION:
; APPLICANT: Agriculture and Agri-Food Canada; The University of Saskatchewan
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Qy 197 GluProLeuGluGlyArgTyrIysTrp 205  
Db 580 ACGCGCTTGAAGTTCGGTACCAGTGG 606

## RESULT 5

US-10-424-599-69339

; Sequence 69339, Application US/10424599

; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 69339

; LENGTH: 1040

; TYPE: DNA

; ORGANISM: Glycine max

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_33625C.1

US-10-424-599-69339

Alignment Scores:  
Pred. No.: 1,15e-13 Length: 1040  
Score: 213.50 Matches: 70  
Percent Similarity: 48.08% Conservative: 30  
Best Local Similarity: 33.65% Mismatches: 67  
Query Match: 20.43% Indels: 41  
DB: 18 Gaps: 8

US-09-980-758A-8 (1-209) x US-10-424-599-69339 (1-1040)

Qy 11 LysLysMetSerGluArgLysArg -----GluLeuAlaGluAlaSer 25  
Db 55 CAGAAATGGGTGATGTAAAGCTCTCTCACAAATGCGCCATAGACACCTTCT 114  
Qy 26 SerThrSerPheSerProLeuLysLysThrLysLysLeuAsnAspSerSerPro 45  
Db 115 TCAAGCCAAACATTCCTATTTCCAGAAAGAAAACACCGCTTCC----- 159  
Qy 46 AspSerHisAspValIleValPheAlaValSerSerSerValAlaSerSerAlaAla 65  
Db 160 -----TTCCAGTTACGCTCTTCCGATACCGAGTTCCTCCGACACT 198  
Qy 66 LeuAlaSerAspGluCysSerValThrIleGlyGlyGluGluSerAspGlnSerSer 85  
Db 199 ATCGTCTCGCGGAAGCTTCGTCAGTTCTACCGC-----ACG 237  
Qy 86 IleSerSerGlyCysPheThrSerGluSerLysGluIleAlaLysAsnSerSerPhe 105  
Db 238 GTTGTTCGGCGAATTTTGTCTCCATCGC-----TCTTGCTGCAGCTCCAGCCAC 288  
Qy 106 GlyValAspLeuGluAspHisGlnIleGluThrGluThrGluThrSerPhe----- 123  
Db 289 TTAAAGACCTC-----CACTCCGTCGCGTCAGATCTGCAGACCAAGGTTTCAAAACG 342  
Qy 124 -----IleThrSerAsnPheArgLysGluThrSerProValSerGluGlyLeuGly 140  
Db 343 GTAGAGGACTCAACCAACCGCTACTCAAGCGGTCAGTTGTTGAGTGAGTTTCTGGA 402  
Qy 141 GluThrThrThrGluMetGluSerSerAlaThrLysArgLysGlnProGlyValArg 160  
Db 403 GACTCGGAGGAATCGCGAAGTCTTCCGCGCAGTGGCGAAA-----TTG 447  
Qy 161 LysThrProThrAlaAlaGluIleGluAspLeuPheSerGluLeuGluSerProAsp 180  
Db 448 AAGACGCCACCAACAGAGAGATCAAGAGATTTTTCGCGATGGCGGAAAGTACGAG--- 504

Qy 181 LysLysLysGlnPheIleGluLysTyrAsnPheAspIleValAsnAspGluProIeuGlu 200  
Db 505 ---CGAAACCGTTTCACAGAGAGTACAACTTTGATATTTGTAGAGATTTGCCGTGGAG 561  
Qy 201 GlyArgTyrLysTrpAspArgLeu 208  
Db 562 GGTGCTACCAGTGGGTTCTGTTTA 585  
RESULT 6  
US-09-733-507-1  
; Sequence 1, Application US/09733507  
; Patent No. US20010025379A1  
; GENERAL INFORMATION:  
; APPLICANT: Agriculture and Agri-Food Canada; The University of Saskatchewan  
; TITLE OF INVENTION: Cyclin Dependant Kinase Inhibitors as Plant Growth  
; TITLE OF INVENTION: Regulators  
; FILE REFERENCE: 81601-3  
; CURRENT APPLICATION NUMBER: US/09/733,507  
; CURRENT FILING DATE: 2000-12-02  
; PRIOR APPLICATION NUMBER: CA 2,256,121  
; PRIOR FILING DATE: 1998-12-31  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 904  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (55)..(627)  
; NAME/KEY: intron  
; LOCATION: (252)..(253)  
; NAME/KEY: intron  
; LOCATION: (296)..(297)  
; NAME/KEY: intron  
; LOCATION: (563)..(564)  
US-09-733-507-1

Alignment Scores:  
Pred. No.: 3.96e-10 Length: 904  
Score: 181.00 Matches: 63  
Percent Similarity: 42.24% Conservative: 35  
Best Local Similarity: 27.16% Mismatches: 68  
Query Match: 17.32% Indels: 66  
DB: 9 Gaps: 10

US-09-980-758A-8 (1-209) x US-09-733-507-1 (1-904)

Qy 5 ProLysAsnProArgGluLysLysMetSerGluArgLysArgGluLeuAlaGluAla 24  
Db 43 CCTAAATCGAAGATGGTCAGAAAATATAGAAAAGCTAAA---GGAATTGTAGAACTGGA 99  
Qy 25 SerSerThrSerPheSerProLeuLysLysThrLysLysLeuAsnAspSerSerAspSer 44  
Db 100 GTTTCGTCAACGTATATGACGTACGAGCCGGAG----- 135  
Qy 45 ProAspSerHisAspValIleValPheAlaValSerSerSerValAlaSerSerAla 64  
Db 136 -----ATTGTTATGTTAGATCGGAAAATCA----- 162  
Qy 65 AlaLeuAlaSerAspGluCysSerValThrIleGlyGlyGluGluSerAspGlnSerSer 84  
Db 163 -----AGCTCTGCTCTCCGTCGCTGAT-----AAT 189  
Qy 85 SerIleSerSerGlyCysPheThrSerGluSerLysGluIleAlaLysAsnSerSerSer 104  
Db 190 GGAGTTTCGTCGCTCTGT-----AGTGAAGCAATGAATATAAGAAAGAAATA--- 240  
Qy 105 PheGlyValAspLeuGluAspHisGlnIleGluThrGluThrGluThrSerThrPhe--- 123  
Db 241 -----ATACATCTGGAGGAGAGATAAAGATGTTGACACTGAAACGTCGACGTATCGA 294  
Qy 124 -----IleThrSerAsnPheArgLysGlu----- 131



[illegible]

## 3

Db 476 AAATTGATGACGGAGATGCCAACCGAATCGGAAATTTGAAGATTTTTTTGTGGAAGCTGAG 535  
 Qy 177 SerProAspAspLysLysLysGlnPheIleGluLysTyrAsnPheAspIleValAsnAsp 196  
 Db 536 AAA-----CAACTCAAGAAGAAATTCAGAAGAAGTACAATTTCGATTTCGAGAAGGAG 589  
 Qy 197 GluProLeuGluGlyArgTyrLysTyrAspArgLeu 208  
 Db 590 AAGCCATTAGAAAGACGTTACGAATGGGTAAAGTTA 625  
 RESULT 8  
 US-10-451-139-18  
 ; Sequence 18, Application US/10451139  
 ; Publication No. US20040098763A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WANG, HONG  
 ; APPLICANT: ZHOU, YONGMING  
 ; APPLICANT: FOWKE, LARRY C.  
 ; APPLICANT: HER MAJESTY IN RIGHT OF CANADA AS REPRESENTED BY THE MINISTER O  
 ; APPLICANT: AGRICULTURE AND AGRIFOOD CANADA  
 ; TITLE OF INVENTION: MODULATION OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR  
 ; TITLE OF INVENTION: ACTIVITY  
 ; FILE REFERENCE: 4810-62237  
 ; CURRENT APPLICATION NUMBER: US/10/451,139  
 ; PRIOR FILING DATE: 2003-06-18  
 ; PRIOR APPLICATION NUMBER: WO PCT/CA01/01825  
 ; PRIOR FILING DATE: 2001-12-18  
 ; PRIOR APPLICATION NUMBER: US 60/255,908  
 ; PRIOR FILING DATE: 2000-12-18  
 ; NUMBER OF SEQ ID NOS: 23  
 ; SOFTWARE: PatentIn ver. 2.0  
 ; SEQ ID NO 18  
 ; LENGTH: 861

CURREN  
PBTOR

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; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,908
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 861
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-451-139-18

Alignment Scores:
Pred. No.: 1,03e-09 Length: 861
Score: 177.00 Matches: 85
Percent Similarity: 51.42% Conservative: 44
Best Local Similarity: 30.66% Mismatches: 73
Query Match: 16.94% Indels: 30
DB: 18 Gaps: 13

US-09-980-758A-8 (1-209) x US-10-451-139-18 (1-861)
Qv 16 ArgLysArgGluLeuAlaGluGluAlaSerThrSerPheSerProLeuLysLysThr 35

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Qy 16 ArgLysArgGluLeuAlaGluGluAlaSerSerThrSerPheSerProLeuLysLysThr 35

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Db 25 AGAGAACGAGATGTTGTTGAAGAGAATCGAGTTACGACG---ACGACGGTGAACACGAGG 81
Qy 36 LysLeuAsnAspSerSerAspSerSerProAspSerHisAspValIleValPheAlaVal 55
Db 82 AAGATGGAGGAGGAAGTGGAT---TTAGTGAATCTAGGATAAATCTCTCCGTTGTGTA 138
Qy 56 SerSerSerSer-----ValAlaSerSerAlaAlaLeuAlaSerAspGluCys 71
Db 139 CAGCGCAGCATCGCGTGGTAATTTGGCGGAGAAATTCAGCAGGAGCGTCGGAGACGAGT 198
Qy 72 SerValThrIleGlyGluGluSer-----ValAlaSerSerAlaAlaLeuAlaSerAspGluCys 81
Db 199 GTTGTATTAGTACGACGCGGAGATCTCTCCGGTTGAAGAACAGTGTCAAATCGAAGAA 258
Qy 82 GlnSerSerSerIleSerSerGlyCysPheThrSerGluSerLysGluIleAlaLysAsn 101
Db 259 GAAGATTCTCGTTCGGTTTCGTGT---TGTCTTACATCGGAAGAGAAA-----TCGAACCGG 309
Qy 102 SerSerSerPheGlyValAspLeuGluAspHisGln---IleGluThrGluThrGluThr 120
Db 310 AGAATCGAATTT---GTAGATCTTGAGGAAATAACCGTGCAGATCTGTGAACAGAAACG 366
Qy 121 SerThrPheIleThrSerAsnPheArgLysGluThrSerProValSerGluGlyLeuGly 140
Db 367 TCG---TCGATTTACCATGATTGAATAAG-----AGTGAGGAATCGATGAACATGGAT 417
Qy 141 GluThrThrThrGluMetGluSerSerSerAlaThrLysArgLysGlnProGlyValArg 160
Db 418 TCTTCTTCGGTGGCTGTTGAAGATGATAGACTCCCGCAGGTTAAGAAAGATCTCCAT 477
Qy 161 LysThrProThrAlaAlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAsp 180
Db 478 GAGACGGTGAAGGAGCTGAGTTAGAACATTTTTCAGGTGGCGGAGAAA-----GAT 531
Qy 181 LysLysLysGlnPheIleGlu-----LysTyrAsnPheAspIleValAsnAspGlu 197
Db 532 CTTCCGAATAAGTTCTTGAATGTTCTATGAAGTATAACTTCGATTTTCGAGAAGATGAG 591
Qy 198 ProLeu---GluGlyArgTyrLysTrpAspArgLeu 208
Db 592 CCACCTTGTGGAGGAAGATACGAGTGGTTAAATTTG 627

RESULT 9
US-10-688-291-1
; Sequence 1, Application US/10688291
; Publication No. US20040073969A1
; GENERAL INFORMATION:
; APPLICANT: De Veylder, Lieven
; APPLICANT: De Almeida, Janice
; APPLICANT: Landrieu, Isabelle
; TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof
; FILE REFERENCE: 1187-2
; CURRENT APPLICATION NUMBER: US/10/688,291
; PRIOR FILING DATE: 2003-10-17
; PRIORITY APPLICATION NUMBER: US/09/526,597D
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 932
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (86)..(712)
US-10-688-291-1
Alignment Scores:
Pred. No.: 1,16e-09 Length: 932
Score: 177.00 Matches: 65
Percent Similarity: 51.42% Conservative: 44
Best Local Similarity: 30.66% Mismatches: 73

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Query Match: 16.94% Indels: 30
DB: 18 Gaps: 13

US-09-980-758A-8 (1-209) x US-10-688-291-1 (1-932)

Qy 16 ArgLysArgGluLeuAlaGluAlaSerSerThrSerPheSerProLeuLysLysThr 35
Db 104 AGAGAACGAGATGTTGTTGAAGAGAATCGAGTTACGACG---ACGACGGTGAACACGAGG 160
Qy 36 LysLeuAsnAspSerSerAspSerSerProAspSerHisAspValIleValPheAlaVal 55
Db 161 AAGATGGAGGAGGAAGTGGAT---TTAGTGAATCTAGGATAAATCTCTCCGTTGTGTA 217
Qy 56 SerSerSerSer-----ValAlaSerSerAlaAlaLeuAlaSerAspGluCys 71
Db 218 CAGCGCAGCAATCCCGTGGTAATTTGGCGGAGAAATTCAGCAGGAGCGTCGGAGACGAGT 277
Qy 72 SerValThrIleGlyGluGluSer-----ValAlaSerSerAlaAlaLeuAlaSerAspGluCys 81
Db 278 GTTGTATTAGTACGACGCGGAGATCTCTCCGGTTGAAGAACAGTGTCAAATCGAAGAA 337
Qy 82 GlnSerSerSerIleSerSerGlyCysPheThrSerGluSerLysGluIleAlaLysAsn 101
Db 338 GAAGATTCTCGTTCGGTTTCGTGT---TGTCTTACATCGGAAGAGAAA-----TCGAACCGG 388
Qy 102 SerSerSerPheGlyValAspLeuGluAspHisGln---IleGluThrGluThrGluThr 120
Db 389 AGAATCGAATTT---GTAGATCTTGAGGAAATAACCGTGCAGATCTGTGAACAGAAACG 445
Qy 121 SerThrPheIleThrSerAsnPheArgLysGluThrSerProValSerGluGlyLeuGly 140
Db 446 TCG---TCGATTTACCATGATTGAATAAG-----AGTGAGGAATCGATGAACATGGAT 496
Qy 141 GluThrThrThrGluMetGluSerSerSerAlaThrLysArgLysGlnProGlyValArg 160
Db 497 TCTTCTTCGGTGGCTGTTGAAGATGATAGACTCCCGCAGGTTAAGAAAGATCTCCAT 556
Qy 161 LysThrProThrAlaAlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAsp 180
Db 557 GAGACGGTGAAGGAGCTGAGTTAGAACATTTTTCAGGTGGCGGAGAAA-----GAT 610
Qy 181 LysLysLysGlnPheIleGlu-----LysTyrAsnPheAspIleValAsnAspGlu 197
Db 611 CTTCCGAATAAGTTGTTGGAATGTTCTATGAAGTATAACTTCGATTTTCGAGAAGATGAG 670
Qy 198 ProLeu---GluGlyArgTyrLysTrpAspArgLeu 208
Db 671 CCACCTTGTGGAGGAAGATACGAGTGGTTAAATTTG 706

RESULT 10
US-10-424-599-67348
; Sequence 67348, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 67348
; LENGTH: 1261
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_3182C.1
US-10-424-599-67348
Alignment Scores:

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Pred. No.: 3 35e-09 Length: 1261
Score: 174.50 Matches: 66
Percent Similarity: 47.39% Conservatives: 43
Best Local Similarity: 28.70% Mismatches: 76
Query Match: 16.70% Indels: 46
DB: 18 Gaps: 9

US-09-980-758A-8 (1-209) x US-10-424-599-67348 (1-1261)

Qy 12 LysMetSerGluArgLysArgGluLeuAlaGluAlaSerSerThrSerPheSerPro 31
Db 176 AAGAAGCGAAGCGAAGGAGAACTCGCGCTCGTCCGATCCACACCAACCAACACC 235
Qy 32 LeuLys-----LysThrLysLeuAsnAspSerSerSerSerPro 45
Db 236 ACCTCCTACATGGGGTCCGAACCGCGCCCAACCCCTAGCGCTTCAGAAATCGCACGG 295
Qy 46 AspSerHisAspValIleValPheAlaValSerSerSerSerValAlaSerSerAlaAl 65
Db 296 CAGCAGCAGCAGCTC-----GCCGCCACTCCGACTCCTACTCCAGCTCCGGAGC 346
Qy 65 aLeuAlaSer----- 68
Db 347 CGTGCCTCCAGAGCGCTCCGATTTTGGTCCACTCTCCGAAGCGCCCTAAGCACCCGAC 406
Qy 69 ----AspGluCysSerValThrIleGlyGluGluSerAspGlnSerSerIleSe 87
Db 407 CCTAAATCCCAATCCCGAAGCTCCAGGCTCGGACTCGCTTCGGAGCGGACGTACC 466
Qy 87 rSerGlyCysPheThrSerGluSerLysGluIleAlaLysAsnSer-----Se 103
Db 467 CTCAC-----ACCACAAACAGAGACAAAT-ACCTTGCATGAGATGCCGACCTCAGAG 519
Qy 103 rSerPheGly-----ValAspLeuGluAspHisGlnIleGluThrGluThr 120
Db 520 GTCGTCGGGGAATGTTTGGATTTTCAAGGTAGAGAGAGACGACTAGGAAATCCAC 579
Qy 120 rSerThrPheIleThrSerAsnPheArgLysGluThrSerProValSerGluGlyLeuGl 140
Db 580 ACCTTGCAGTTTGTAAAGGACTCGGATACTGTCTCAGGACTCCG-----GG 624
Qy 140 vGluThrThrThrGluMetGluSerSerSerAlaThrLysArgLysGlnProGlyValAr 160
Db 625 TTCACTACAGCGCTACTGTTGTAGCTGAAGCTTATCGAAGAACACAGACATGCGAGTAC 684
Qy 160 gLys---ThrProThrAlaAlaGluIleGluAspLeuPheSerGluLeuGluSerProAs 179
Db 685 AAGCAAAATCCCACTCCCGTGAATGGATGTAATCTTGTGAAATGAAGAGGCTCA 744
Qy 179 pAspLysLysLysGlnPheIleGluLysTyraenPheAspIleValAsnAspGluProle 199
Db 745 GCAAAAAA-----TTCATTGAGAAGTACAACTTTGATCCTGCTGATGAGAAAGCGCT 798
Qy 199 uGluGlyArgTyraenPheAspArgLeu 208
Db 799 CTCAGGCGCTATGAATGGAAGTTG 826

RESULT 11
US-09-733-507-3
; Sequence 3, Application US/09733507
; Patent No. US2001002579A1
; GENERAL INFORMATION:
; APPLICANT: AGRICULTURE AND AGRI-FOOD CANADA
; APPLICANT: FOWKE, LARRY C.
; APPLICANT: ZHOU, YONGMING
; APPLICANT: HER MAJESTY IN RIGHT OF CANADA AS REPRESENTED BY THE MINISTER OF
; APPLICANT: AGRICULTURE AND AGRI-FOOD CANADA
; TITLE OF INVENTION: CYCLIN DEPENDANT KINASE INHIBITORS AS PLANT GROWTH
; TITLE OF INVENTION: MODULATION OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR
; FILE REFERENCE: 4810-62237
; CURRENT APPLICATION NUMBER: US/10/451,139
; PRIOR FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: WO PCT/CA01/01825
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,908
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3

US-10-451-139-3
; Sequence 3, Application US/10451139
; Publication No. US20040098763A1
; GENERAL INFORMATION:
; APPLICANT: WANG, HONG
; APPLICANT: ZHOU, YONGMING
; APPLICANT: FOWKE, LARRY C.
; APPLICANT: HER MAJESTY IN RIGHT OF CANADA AS REPRESENTED BY THE MINISTER OF
; APPLICANT: AGRICULTURE AND AGRI-FOOD CANADA
; TITLE OF INVENTION: CYCLIN DEPENDANT KINASE INHIBITORS AS PLANT GROWTH
; TITLE OF INVENTION: MODULATION OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR
; FILE REFERENCE: 4810-62237
; CURRENT APPLICATION NUMBER: US/10/451,139
; PRIOR FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: WO PCT/CA01/01825
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,908
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3

```

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; LENGTH: 660
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-733-507-3

Alignment Scores:
Pred. No.: 1 54e-09 Length: 660
Score: 174.00 Matches: 52
Percent Similarity: 46.67% Conservatives: 25
Best Local Similarity: 31.52% Mismatches: 48
Query Match: 16.65% Indels: 40
DB: 9 Gaps: 7

US-09-980-758A-8 (1-209) x US-09-733-507-3 (1-660)

Qy 72 SerValThrIleGlyGluGluSerAspGlnSerSerSerIleSerSerGlyCysPhe 91
Db 58 TCTGTCTCGTCTCGTCTCGTCTCGTCTCGTCTCGTCTCGTCTCGTCTCGTCTCGTCT 99
Qy 92 ThrSerGluSerLysGluIleAlaLysAsnSerSerSerPheGlyValAspLeuGluApp 111
Db 100 ---AGTGAAGCAATGAAATATATAAGAAAGAAAGAAATTA-----ATACATCTGGAGGAG 147
Qy 112 HisGlnIleGluThrGluThrGluThrSerThrPhe-----Ile 124
Db 148 GAAGATAAGATGGTGCACACTGAAACGTCGACGTATCGACGGGTACGAGAGGAAGCTT 207
Qy 125 ThrSerAsnPheArgLysGlu----- 131
Db 208 TTTGAAATCTCAGAGAGAGGAGAGAAAGAAAGAAATTAAGTAAATCCATGGAGAATTATTCA 267
Qy 132 -----ThrSerProValSerGluGlyLeu-----GlyGluThrThr 143
Db 268 TCGGAATTTGAATCCGCGGTTAAAGAAATCGTTAGATTGTTGTAGCGGAGGAGAAACG 327
Qy 144 ThrGluMetGluSerSerSerAlaThrLysArgLysGlnProGlyValArgLysThrPro 163
Db 328 ATGAGGAGAGCGTACGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 387
Qy 164 ThrAlaAlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAspLysLysLys 183
Db 388 ACGGAATCGGAATTTGAAGATTTTGTGGAAGCTGAGAAA-----CAACTCAAGAA 441
Qy 184 GlnPheIleGluLysTyraenPheAspIleValAsnAspGluProLeuGluGlyArgTy 203
Db 442 AAATTCAGAAAGAGTACAAATTTTCGATTTCGAGAAGGAGAGAGCCATTAGAGGACGTTAC 501
Qy 204 LysTTPAspArgLeu 208
Db 502 GAATCGGTAAAGTTA 516

RESULT 12
US-10-451-139-3
; Sequence 3, Application US/10451139
; Publication No. US20040098763A1
; GENERAL INFORMATION:
; APPLICANT: WANG, HONG
; APPLICANT: ZHOU, YONGMING
; APPLICANT: FOWKE, LARRY C.
; APPLICANT: HER MAJESTY IN RIGHT OF CANADA AS REPRESENTED BY THE MINISTER OF
; APPLICANT: AGRICULTURE AND AGRI-FOOD CANADA
; TITLE OF INVENTION: CYCLIN DEPENDANT KINASE INHIBITORS AS PLANT GROWTH
; TITLE OF INVENTION: MODULATION OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR
; FILE REFERENCE: 4810-62237
; CURRENT APPLICATION NUMBER: US/10/451,139
; PRIOR FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: WO PCT/CA01/01825
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,908
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3

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; LENGTH: 660
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-451-139-3

Alignment Scores:
Pred. No.: 1.54e-09 Length: 660
Score: 174.00 Matches: 52
Percent Similarity: 46.67% Conservative: 25
Best Local Similarity: 31.52% Mismatches: 48
Query Match: 16.65% Indels: 40
DB: 18 Gaps: 7

US-09-980-758A-8 (1-209) x US-10-451-139-3 (1-660)
Qy 72 SerValThrIleGlyGluGluSerAspGlnSerSerSerIleSerSerGlyCysPhe 91
Db 58 TCTGTCCTCCGTCGTCGGTAT-----AATGGAGTTTCGTCTTGT--- 99
Qy 92 ThrSerGluSerLysGluIleAlaLysAsnSerSerPheGlyValAspLeuGluAsp 111
Db 100 ---AGTGAAGCAATATATAAGAAAGAAATTA-----ATACATCTGGAGGAG 147
Qy 112 HisGlnIleGluThrGluThrSerThrPhe-----Ile 124
Db 148 GAAGATAAAGATGTTGCACACTGAACGTCGACGTATCGACGGGTATCGAAGAGGAAGCTT 207
Qy 125 ThrSerAsnPheArgLysGlu----- 131
Db 208 TTTGAAATCTGAGAGAGGAGGAGAAAGAAATTAATCAATCGAGAAATTATTCA 267
Qy 132 -----ThrSerProValSerGluGlyLeu-----GlyGluThrThr 143
Db 268 TCGGAATTGTAATCGCGCGTTAAAGATCGTTAGATTGTTGTAGCGGGAGGAAACG 327
Qy 144 ThrGluMetGluSerSerAlaThrLysArgLysGlnProGlyValArgLysThrPro 163
Db 328 ATGGAGGAGACGTCACGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 387
Qy 164 ThrAlaAlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAspLysLysLys 183
Db 388 ACGGAATCGGAATTTGAAGATTTTTTTGTGGAAGCTGAGAAA-----CAACTCAAGAA 441
Qy 184 GlnPheIleGluLysTyrAsnPheAspIleValAsnAspGluProLeuGluGlyArgTyr 203
Db 442 AAATTCAAGAGAAGTACAAATTCGATTTCGAGAGAGGAGAGCCATTAGAGGCGTTAC 501
Qy 204 LysTrpAspArgLeu 208
Db 502 GAATGGGTAAAGTTA 516

RESULT 13
US-10-424-599-40086
; Sequence 40086, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Zhou Yihua
; APPLICANT: Kovalic David K
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 40086
; LENGTH: 1237
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_136198C.1
US-10-424-599-40086
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Alignment Scores:
Pred. No.: 6.2e-09 Length: 1237
Score: 172.00 Matches: 63
Percent Similarity: 48.29% Conservative: 36
Best Local Similarity: 30.73% Mismatches: 74
Query Match: 16.46% Indels: 32
DB: 18 Gaps: 10

US-09-980-758A-8 (1-209) x US-10-424-599-40086 (1-1237)
Qy 20 LeuAlaGluGluAlaSerSerThrSerPheSerProLeuLysLysThrLysLeuAsnAsp 39
Db 318 TTAGCCATGGAAGCTGTAGTTCTGCTGAACCATCATCCAGAGAGAAAGAGATCAGCAAC 377
Qy 40 SerSerAspSerProAspSerHisAspValIleValPheAlaValSerSerSerSer 59
Db 378 AGTACTAACCAAGACCAAAA-----CTCTCCCAAGACT 410
Qy 60 ValAlaSerSerAlaAlaLeuAlaSerAspGluCysSerValThrIleGlyGluGlu 79
Db 411 CCGAGAACGAGATTCTCTCGCTGTCAAAACGACGCGGTGACG-----GAG 458
Qy 80 SerAspGlnSerSer-----IleSerSerGlyCysPheThrSerGluSerLys 96
Db 459 ATGTTTCAGCGCGTGTCTCGGAGATGTTTCAGCAACGCTGCTGAGCCCTACCTCCAGT 518
Qy 97 GluIle-----AlaLysAsnSerSerPheGlyValAsp----- 108
Db 519 GAAATTCGGCGCTTCTGCTGCTCCAGCAACGGATCCATTGGCCTCGATCAGGACGAGATC 578
Qy 109 ---LeuGluAspHisGlnIleGluThr---GluThrGluThrSerThrPheIleThrSer 126
Db 579 AAGCTCTTAGATCTGGAGGTGAGAGCGCGCAAGTTGAAACGTCGACGTGCAATGGTGGT 638
Qy 127 Asn-----PheArgLysGluThrSerProValSerGluGlyLeuGlyGluThrThr 144
Db 639 CATGAAATTCAGAGAGAGAGAGATGAAACGTTTCCAGCGAG---CTTCGCGAGATTTCTCAG 695
Qy 145 GluMetGluSerSerSerAlaThrLysArgLysGlnProGlyValArgLysThr---Pro 163
Db 696 GAGCGGAGGCCAATGGAGATCAATCTCACCGTCTTATCAAGGCAAAAGCCATGCCT 755
Qy 164 ThrAlaAlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAspLysLysLys 183
Db 756 ACCGAATTGGAGCTCGAGGAATTTCTGCTGCTCGGAGAAA-----GACATTCAGAAA 809
Qy 184 GlnPheIleGluLysTyrAsnPheAspIleValAsnAspGluProLeuGluGlyArgTyr 203
Db 810 CGATTTCAAGACAGATACAATTATGATATTGTTAAGGACGCTACCGCTGGAAGGACGCTAC 869
Qy 204 LysTrpAspArgLeu 208
Db 870 GAGTGGGTTCAGTTG 884

RESULT 14
US-09-733-507-15
; Sequence 15, Application US/09733507
; Patent No. US20010025379A1
; GENERAL INFORMATION:
; APPLICANT: Agriculture and Agri-Food Canada; The University of Saskatchewan
; TITLE OF INVENTION: Cyclin Dependant Kinase Inhibitors as Plant Growth
; TITLE OF INVENTION: Regulators
; FILE REFERENCE: 81601-3
; CURRENT APPLICATION NUMBER: US/09/733,507
; CURRENT FILING DATE: 2000-12-02
; PRIOR APPLICATION NUMBER: CA 2,256,121
; PRIOR FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 804
; TYPE: DNA
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; ORGANISM: Chenopodium rubrum
US-09-733-507-15

Alignment Scores:
Pred. No.: 8,33e-09      Length: 804
Score: 168.50           Matches: 61
Percent Similarity: 41.67%      Conservative: 34
Best Local Similarity: 26.75%    Mismatches: 66
Query Match: 16.12%             Indels: 67
DB: 9                     Gaps: 10

US-09-980-758A-8 (1-209) x US-09-733-507-15 (1-804)

QY 15 GluArgLysArgGluLeuAlaGluAlaSerSerThr---SerPheSerProLeuLys 33
DB 37 GAGCTCGAGACTGCCCTAGCTATGCGCGCAGCTGTACTCCAACCTTCGCTCCGCGGAAG 96
QY 34 LysThrLysLeuAsnAspSerSerAsp----- 42
DB 97 AAGATCAAGAGGTTTCGAGTCGCTATATATTCCTCAACTAAGAGTCGTCGAAAG 156
QY 43 -----SerSerProAspSerHisAspValIleValPheAlaValSerSerSerVal 60
DB 157 AATTTGTCGCGCGCGAGAAAT-----TTCCGCGAAATTAGAAACGACGCCG 201
QY 75 IleGlyGlyGluSerLysGluLeuAlaLysSerSerSerSerSerSerSerSerSerSer 74
DB 262 ATTACTACAGTAGTCGAGATTTTCGCGCGCTTGTGCTCAAGCAATTATGATCAGTTG 321
QY 92 ThrSerGluSerLysGluLeuAlaLysAsnSerSerSerSerSerSerSerSerSerSer 111
DB 322 AGTTCTAGCGAGCCAGAGTAGTTAAGGATGATGATGTTTTCGCGAAATCGTACAGCAGAT 381
QY 112 HisGlnIleGluThrGluThrGluThrSerThrPheIleThrSerAsnPheArgLysGlu 131
DB 382 CCAGAGGTTGAGAGT-----GTTGAGGCGCTCGTCAAGCAAAAGAGAGCCATAGA 396
QY 132 ThrSerProValSerGluGlyLeuGlyGluThrThrGluMetGluSerSerSerAla 151
DB 397 -----GTTGAGGCGCTCGTCAAGCAAAAGAGAGCCATAGA 432
QY 152 ThrLysArgLysGln-----ProGlyValArgLysThr 162
DB 433 ACAGAAGCGAGAGAGCTACAAAATTAGACGACGAGGATTATCCGCGCAGCAAAATCAACG 492
QY 163 -----ProThrAlaAlaGluIleGluAAspLeuPheSerGluLeuGluSer 177
DB 493 GTACAGATCAAGATCCGCTCTGATTTCAGAAATCGAAGAAATCTTGTGCTGCTGAAAAA 552
QY 178 ProAspAspLysLysGlnPheIleGluLysTyrAsnPheAspIleValAsnAspGlu 197
DB 553 -----GATCTCCAGAAACGCTTCAGCGAAAGATACAAATTCGACATAGTTAAGGACGTG 606
QY 198 ProLeuGluGlyArgTyrLysTyr 205
DB 607 CCACTGAAAGGTCGTTATGATTGG 630

RESULT 15
US-10-451-139-14
; Sequence 14, Application US/10451139
; Publication No. US20040098763A1
; GENERAL INFORMATION:
; APPLICANT: WANG, HONG
; APPLICANT: ZHOU, YONGMING
; APPLICANT: FOWKE, LARRY C.
; APPLICANT: HER MAJESTY IN RIGHT OF CANADA AS REPRESENTED BY THE MINISTER OF
; APPLICANT: AGRICULTURE AND AGRI-FOOD CANADA
; TITLE OF INVENTION: MODULATION OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR
; TITLE OF INVENTION: ACTIVITY

```

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; FILE REFERENCE: 4810-62237
; CURRENT APPLICATION NUMBER: US/10/451,139
; PRIOR FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: WO PCT/CA01/01825
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,908
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 804
; TYPE: DNA
; ORGANISM: Chenopodium rubrum
US-10-451-139-14

Alignment Scores:
Pred. No.: 8,33e-09      Length: 804
Score: 168.50           Matches: 61
Percent Similarity: 41.67%      Conservative: 34
Best Local Similarity: 26.75%    Mismatches: 66
Query Match: 16.12%             Indels: 67
DB: 18                     Gaps: 10

US-09-980-758A-8 (1-209) x US-10-451-139-14 (1-804)

QY 15 GluArgLysArgGluLeuAlaGluAlaSerSerThr---SerPheSerProLeuLys 33
DB 37 GAGCTCGAGACTGCCCTAGCTATGCGCGCAGCTGTACTCCAACCTTCGCTCCGCGGAAG 96
QY 34 LysThrLysLeuAsnAspSerSerAsp----- 42
DB 97 AAGATCAAGAGGTTTCGAGTCGCTATATATTCCTCAACTAAGAGTCGTCGAAAG 156
QY 43 -----SerSerProAspSerHisAspValIleValPheAlaValSerSerSerVal 60
DB 157 AATTTGTCGCGCGCGAGAAAT-----TTCCGCGAAATTAGAAACGACGCCG 201
QY 61 AlaSerSerAlaAlaLeuAlaSerSerAspGlu-----CysSerValThr 74
DB 202 TTGGAAGTTGCGCGCGTGTTCGAGGAGGAAGAGGTTGCGAAATTGCTCGAGTAGCAGGTA 261
QY 75 IleGlyGlyGluSerLysGluLeuAlaLysSerSerSerSerSerSerSerSerSerSer 91
DB 262 ATTACTACAGTAGTCGAGATTTTCGCGCGCTTGTGCTCAAGCAATTATGATCAGTTG 321
QY 92 ThrSerGluSerLysGluLeuAlaLysAsnSerSerSerSerSerSerSerSerSerSer 111
DB 322 AGTTCTAGCGAGCCAGAGTAGTTAAGGATGATGATGTTTTCGCGAAATCGTACAGCAGAT 381
QY 112 HisGlnIleGluThrGluThrGluThrSerThrPheIleThrSerAsnPheArgLysGlu 131
DB 382 CCAGAGGTTGAGAGT-----GTTGAGGCGCTCGTCAAGCAAAAGAGAGCCATAGA 396
QY 132 ThrSerProValSerGluGlyLeuGlyGluThrThrGluMetGluSerSerSerAla 151
DB 397 -----GTTGAGGCGCTCGTCAAGCAAAAGAGAGCCATAGA 432
QY 152 ThrLysArgLysGln-----ProGlyValArgLysThr 162
DB 433 ACAGAAGCGAGAGAGCTACAAAATTAGACGACGAGGATTATCCGCGCAGCAAAATCAACG 492
QY 163 -----ProThrAlaAlaGluIleGluAAspLeuPheSerGluLeuGluSer 177
DB 493 GTACAGATCAAGATCCGCTCTGATTTCAGAAATCGAAGAAATCTTGTGCTGCTGAAAAA 552
QY 178 ProAspAspLysLysGlnPheIleGluLysTyrAsnPheAspIleValAsnAspGlu 197
DB 553 -----GATCTCCAGAAACGCTTCAGCGAAAGATACAAATTCGACATAGTTAAGGACGTG 606
QY 198 ProLeuGluGlyArgTyrLysTyr 205
DB 607 CCACTGAAAGGTCGTTATGATTGG 630

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Search completed: September 30, 2005, 14:08:48  
Job time : 660 secs

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 30, 2005, 11:36:09 ; Search time 3168 Seconds  
(without alignments)  
2511.184 Million cell updates/sec

Title: US-09-980-758A-8  
Perfect score: 1045  
Sequence: 1 PRDLPKNREKQMSERKEL.....NFDIVNDFLEGRYKWDRLX 209

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-Q=/cgn2\_1/USPTO\_spool/US09980758/runat\_30092005\_100632\_520/app\_query.fasta\_1.391  
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0 -L-LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45  
-LOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09980758 @CGN\_1\_1\_4352 @runat\_30092005\_100632\_520 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:\*  
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2: gb\_est2:\*  
3: gb\_htc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_ges1:\*  
9: gb\_ges2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1007	96.4	797	CNS0A7OL	BX826283 Arabidops
2	991	94.8	893	CNS0A6HI	BX825232 Arabidops
3	923	88.3	664	AU237797	AU237797 Arabidops
4	900	86.1	736	CNS0A6EV	BX826140 Arabidops
5	874	83.6	784	CNS0A6EQ	BX825610 Arabidops
6	492.5	47.1	457	BX840619	BX840619 Arabidops
7	365	34.9	425	AU228889	AU228889 Arabidops
8	306	29.3	654	BZ426940	BZ426940 Arabidops
9	305	29.2	831	BH708120	BH708120 Arabidops

10	298.5	28.6	700	8	BZ083701	BZ083701 lxx95all.
11	246	23.5	646	1	AI728644	AI728644 BNLGH1112
12	241.5	23.1	794	6	CB288800	CB288800 V-B-19C02
13	239	22.9	919	7	CV242992	CV242992 WS02516.B
14	238.5	22.8	888	7	CF212120	CF212120 CGF100066
15	224	21.4	808	6	CD574460	CD574460 UCRPT01.0
16	223.5	21.4	902	5	BQ794660	BQ794660 EST_3598
17	223	21.3	672	7	CO098695	CO098695 GR_Ba23C
18	223	21.3	747	7	CF212022	CF212022 CGF100066
19	223	21.3	774	7	CF212022	CF212022 VRSK512T7
20	222.5	21.3	722	7	CO070046	CO070046 GR_Ba260
21	222.5	21.3	815	7	CO079309	CO079309 GR_Ba42A
22	219	21.0	747	7	CO408371	CO408371 VRSK512 Vi
23	218.5	20.9	712	7	CV234322	CV234322 WS01214.B
24	214.5	20.5	777	7	CO079308	CO079308 GR_Ba42A
25	214	20.5	817	7	CK934305	CK934305 CGF100426
26	214	20.5	846	7	CK934861	CK934861 CGF100422
27	214	20.5	878	6	CD574461	CD574461 UCRPT01.0
28	209	20.0	815	7	CK934419	CK934419 CGF100425
29	203	19.4	701	7	CV084380	CV084380 Mdbb5027P
30	199	19.0	593	7	CN940550	CN940550 010913ABV
31	193.5	18.5	592	7	CN912198	CN912198 021717ABM
32	193.5	18.5	945	7	CV280994	CV280994 WS0138.B2
33	188	18.0	852	7	CO121570	CO121570 GR_Bb02N
34	187	17.9	910	7	CV280549	CV280549 WS0136.B2
35	186.5	17.8	885	7	CK136404	CK136404 MM2_1.4.C
36	184	17.6	709	5	BU009283	BU009283 QGJ10A12.
37	183.5	17.6	408	5	BP670981	BP670981 BP670981
38	183.5	17.6	707	5	BU862176	BU862176 S012D05.P
39	183	17.5	602	5	BQ863066	BQ863066 QGC22002.
40	180	17.2	607	7	CK665094	CK665094 USDA.FP3
41	180	17.2	1017	5	BQ481784	BQ481784 PV_Gea010
42	179	17.1	623	2	BE347049	BE347049 sp34609.Y
43	179	17.1	862	7	CV256047	CV256047 WS0242.B2
44	178	17.0	569	5	BQ872660	BQ872660 QG116E20.
45	177.5	17.0	445	7	CF234588	CF234588 PcaJXT001

#### ALIGNMENTS

CNS0A7OL 797 bp mRNA linear HTC 06-FEB-2004  
Arabidopsis thaliana Full-length cDNA Complete sequence from clone  
GSLTSL92805 of Silique of strain col-0 of Arabidopsis thaliana  
(thale cress).  
BX826283 1 GI:42466833  
HTC; GSLT cDNA.  
Arabidopsis thaliana (thale cress)  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 797)  
Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,  
Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,  
Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.  
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:  
A Combined Approach to Evaluate and Improve Arabidopsis Genome  
Annotation  
Unpublished  
2 (bases 1 to 797)  
Genoscope.  
Direct Submission  
Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)  
- Web : www.genoscope.cns.fr  
The sequences are based on single pass reads.  
Life Technologies (a division of Invitrogen) members carried out  
full-length libraries construction : Temple G.  
Genoscope members carried out sequencing and annotation : Castelli  
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,

Schachter V., Weissenbach J., Salanoubat M.  
 URGV INRA : Clepet C., Caboche M.  
 Annotation is based on the June 2003 version of the Arabidopsis  
 genome released by MIPS (Munich Information center for Protein  
 Sequences). 5 prime and 3 prime are assembled with Phrap.  
[http://www.genoscope.cns.fr/externe/sequences/Banque\\_Projet\\_EF/Full\\_length](http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full_length)  
<http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis>.

## FEATURES

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1. 797  
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 /strain="Col-0"  
 /db\_xref="taxon:3702"  
 /clone="GSLTSL192805"  
 /tissue\_type="Silique"  
 /plasmid="pCMVSPORT\_6"  
 complement(1..797)  
 /gene="At3g19150"

## gene

## ORIGIN

Alignment Scores:  
 Pred. No.: 2,128-96 Length: 797  
 Score: 1007.00 Matches: 202  
 Percent Similarity: 99.51% Conservative: 0  
 Best Local Similarity: 99.51% Mismatches: 1  
 Query Match: 96.36% Indels: 0  
 DB: 3 Gaps: 0

US-09-980-758A-8 (1-209) x CNS0A70L (1-797)

QY 6 LysAenProArgGluLysMetSerGluArgLysArgGluLeuAlaGluAlaSer 25  
 DB 2 AAAAAATCCAGAGAGAAAAAATGAGCGAGAGAAAGCGAGCTTGCAGAGAGCTTCA 61  
 QY 26 SerThrSerPheSerProLeuLysLysThrLysLeuAenAspSerSerAspSerPro 45  
 DB 62 AGCACAAGCTCTTCAACCACTGAAGAAAAACGAAGCTTAATGATTTCTCTGATTCATCACCG 121  
 QY 46 AspSerHisAspValIleValPheAlaValSerSerSerSerValAlaSerSerAlaAla 65  
 DB 122 GACTCTCATGACGTCACTCGCTTCGCGGTTCATCTTCTCGTTCGTCGCGGCT 181  
 QY 66 LeuAlaSerAspGluCysSerValThrIleGlyGlyGluGluSerAspGlnSerSerSer 85  
 DB 182 TTAGCGTCTGATGATGTTCCGTTACCATCGGTGAGAGAAAGTGATCAGTCTCGAGT 241  
 QY 86 IleSerSerGlyCysPheThrSerGluSerLysGluIleAlaLysAenSerSerPhe 105  
 DB 242 ATCAGCTCCGGTGTGTTCCACCACTGAATCGAAAGAAATCGCGAAGACAGTTCGTCGTT 301  
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 QY 126 SerAenPheArgLysGluThrSerProValSerGluGlyLeuGlyGluThrThrThrGlu 145  
 DB 362 AGCAATTTCAAGAGAGACGNGTCCAGTGAGTGGGAGTGGGAGAACGACACAGAA 421  
 QY 146 MetGluSerSerSerAlaThrLysArgLysGlnProGlyValArgLysThrProThrAla 165  
 DB 422 ATGGAATCATCATCGCAACGAAGAGAAAAACAACCGGGGGTGGAGAACTCCAAACGCG 481  
 QY 166 AlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAspLysValGlnPhe 185  
 DB 482 GCGGAGATTGAGGATTTGTTCTCGGAGCTAGAGATCAAGAGATGAAGAAGCAATTC 541  
 QY 186 IleGluLysYrAsnPheAspIleValAenAspGluProLeuGluGlyArgTyrIleYrP 205  
 DB 542 ATAGAAAAGTACAACCTTCGATATTGTCATGACGAACCGCTTGAAGGTCGCTACAGTGG 601  
 QY 206 AspArgLeu 208  
 |||||

DB 602 GATCGACTT 610  
 RESULT 2  
 CNS0A6HI  
 LOCUS  
 DEFINITION  
 CNS0A6HI 893 bp mRNA linear HTC 06-FEB-2004  
 Arabidopsis thaliana Full-length cDNA complete sequence from clone  
 GSUTSL212F04 of Silique of strain col-0 of Arabidopsis thaliana  
 (thale cress).  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Arabidopsis thaliana (thale cress)  
 Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 The sequences are based on single pass reads.  
 Life Technologies (a division of Invitrogen) members carried out  
 full-length libraries construction : Temple G.  
 Genoscope members carried out sequencing and annotation : Castelli  
 V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,  
 Schachter V., Weissenbach J., Salanoubat M.  
 URGV INRA : Clepet C., Caboche M.  
 Annotation is based on the June 2003 version of the Arabidopsis  
 genome released by MIPS (Munich Information center for Protein  
 Sequences). 5 prime and 3 prime are assembled with Phrap.  
[http://www.genoscope.cns.fr/externe/sequences/Banque\\_Projet\\_EF/Full\\_length](http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full_length)  
<http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis>.  
 Location/Qualifiers  
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 /db\_xref="taxon:3702"  
 /clone="GSLTSL212F04"  
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 /plasmid="pCMVSPORT\_6"  
 complement(1..893)  
 /gene="At3g19150"

## ORIGIN

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 Best Local Similarity: 98.03% Mismatches: 2  
 Query Match: 94.83% Indels: 0  
 DB: 3 Gaps: 0

US-09-980-758A-8 (1-209) x CNS0A6HI (1-893)

QY 6 LysAenProArgGluLysLysMetSerGluArgLysArgGluLeuAlaGluAlaSer 25  
 DB 2 AAAAAATCCAGAGAGAAAAAATGAGCGAGAGAAAGCGAGCTTGCAGAGAGCTTCA 61  
 QY 26 SerThrSerPheSerProLeuLysLysThrLysLeuAenAspSerSerAspSerPro 45  
 DB 62 AGCACAAGCTTCTCACCACTGAAGAAAAACGAAGCTTAATGATTTCTTCTGATTCATCACCG 121



QY 46 AspSerHisAspValIleValPheAlaValSerSerSerValAlaSerSerAlaAla 65  
 DB 122 GACTCTCATGACGTATCGTCTCGGGTTTCACTCTCTCGTTCGTCGGCGCT 181  
 QY 66 LeuAlaSerAspGluCysSerValThrIleGlyGlyGluGluSerAspGlnSerSer 85  
 DB 182 TTACGCTCTGATGAATGTTCCGTTACCATCGGTGGAGAAAGTGTATCATCTCGAGT 241  
 QY 86 IleSerSerGlyCysPheThrSerGluSerLysGluIleAlaLysAsnSerSerPhe 105  
 DB 242 ATCAGCTCCGGTTGTTTCCACAGTGAATCGAAGAAATCGGAAGACAGTTCGTCGTT 301  
 QY 106 GlyValAspLeuGluAspHisGlnIleGluThrGluThrGluThrSerThrPheIleThr 125  
 DB 302 GGTGTAGATCTGGAGATCATCAATCGAAACCGAAACCGAAACCTCAACATTCATCACC 361  
 QY 126 SerAsnPheArgLysGluThrSerProValSerGluGlyLeuGlyGluThrThrGlu 145  
 DB 362 AGCAATTTGAGAAAGAGAGAGTCCAGTGAGTGAAGGTTTGGAGAAACGACACAGAA 421  
 QY 146 MetGluSerSerSerAlaThrLysArgLysGlnProGlyValArgLysThrProThrAla 165  
 DB 422 ATGGAATCATATCGCAACGAGAGAAACAAACCGGGGTGAGGAAGACTCCCAACGGCG 481  
 QY 166 AlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAspLysLysLysGlnPhe 185  
 DB 482 GCGGAGATTTAGGATTTGTTCTCGGAGCTACAGATCAAGACGATAGAAGAACGAAATTC 541  
 QY 186 IleGluLysTyrAsnPheAspIleValAsnAspGluProLeuGluGlyValArgTyrLysTrp 205  
 DB 542 ATAGAAAAGTACAACTTCGATATTGTAATGACGAACCGCTTGAAGTCTCGTACAAGTG 601  
 QY 206 AspArgLeu 208  
 DB 602 GATCGACTT 610

RESULT 3  
 AU237797  
 LOCUS AU237797 RAFL16 Arabidopsis thaliana cDNA clone RAFL16-57-G19 5',  
 DEFINITION mRNA sequence.  
 ACCESSION AU237797.1 GI:19876966  
 VERSION AU237797  
 KEYWORDS EST.  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi  
 1 (bases 1 to 664)  
 Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,  
 Akiyama,K., Enju,A., Oono,Y., Sakurai,T., Carninci,P., Kawai,J.,  
 Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A.,  
 Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.  
 Large scale analysis of Arabidopsis full-length cDNA  
 Unpublished (2002)  
 Contact: Motoaki Seki  
 Plant Functional Genomics Research Group  
 RIKEN Genomic Sciences Center  
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
 Tel: 81-298-36-4359  
 Fax: 81-298-36-9060  
 Email: mseki@tc.riken.go.jp  
 An Arabidopsis full-length cDNA library was constructed essentially  
 as reported previously (Seki et al., 1998). cDNA cleaved with BamHI  
 and XhoI was ligated to modified Lambda PLC-1 vector (Carninci et  
 al., submitted for publication) digested with BamHI and SalI. This  
 clone is in a modified pBluescript vector. Please visit our web  
 site ([http://www.gsc.riken.go.jp/e/plant/index\\_e.html](http://www.gsc.riken.go.jp/e/plant/index_e.html)) for further  
 details.  
 FEATURES  
 Location/Qualifiers  
 source 1..664

/organism="Arabidopsis thaliana"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3702"  
 /clone="RAFL16-57-G19"  
 /lab\_host="DH10B"  
 /clone\_lib="RAFL16"  
 /note="Site\_1: BamHI; Site\_2: SalI; dark-grown"

ORIGIN

Alignment Scores:  
 Pred. No.: 1,37e-87 Length: 664  
 Score: 923.00 Matches: 192  
 Percent Similarity: 96.06% Conservative: 3  
 Best Local Similarity: 94.58% Mismatches: 8  
 Query Match: 88.33% Indels: 1  
 DB: 1 Gaps: 0  
 US-09-980-758A-8 (1-209) x AU237797 (1-664)  
 QY 6 LysAsnProArgGluLysLysMetSerGluAArgLysArgGluLeuAlaGluAlaSer 25  
 DB 20 AAAAAATCCAGAGAGAGAAAAAATGACGAGAGAGAAAGCGAGAGCTTCAGAGAAGCTTCA 79  
 QY 26 SerThrSerPheSerProLeuLysLysThrLysLeuAsnAspSerSerAspSerPro 45  
 DB 80 AGCACAAAGCTTCTCACCACTGAAGAAACGAAGCTTAAATGATCTTCTGATTCATCACCG 139  
 QY 46 AspSerHisAspValIleValPheAlaValSerSerSerValAlaSerSerAlaAla 65  
 DB 140 GACTCTCATGACGTATCGTCTCGCGTTTCATCTCTTCGTCGTCGTCGCGGCT 199  
 QY 66 LeuAlaSerAspGluCysSerValThrIleGlyGlyGluGluSerAspGlnSerSer 85  
 DB 200 TTAGCGTCTGATGAATGTTCCGTTACCATCGGTGGAGAAAGAGTGTATCATCTCGAGT 259  
 QY 86 IleSerSerGlyCysPheThrSerGluSerLysGluIleAlaLysAsnSerSerPhe 105  
 DB 260 ATCAGCTCCGGTTGTTTCCACAGTGAATCGAAAGAAATCTCGAAGAACAGTTCGTCGTT 319  
 QY 106 GlyValAspLeuGluAspHisGlnIleGluThrGluThrGluThrSerThrPheIleThr 125  
 DB 320 GGTGTAGATCTCGAGGATCATCAATCGAAACCGAAACCGAAACCTCAACATTCATCACC 379  
 QY 126 SerAsnPheArgLysGluThrSerProValSerGluGlyLeuGlyGluThrThrGlu 145  
 DB 380 AGCAATTTTCAGAAAAAGAGACGAGTCCAGTGAAGGGTTTGGGAGAAACGACACAGAA 439  
 QY 146 MetGluSerSerSerAlaThrLysArgLysGlnProGlyValArgLysThrProThrAla 165  
 DB 440 ATGGAATCATATCGCGCAACGAGAGAAACACCGGGGTGAGGAAGACTCCCAACGGCG 499  
 QY 166 AlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAspLysLysGlnPhe 185  
 DB 500 GCGGAGATTGAGGATTGTTCTCGGAGCTAGAGAGTCAAGACGATNAGAAGAAAGCAATTC 559  
 QY 186 IleGluLysTyrAsnPheAspIleValAsnAspGluProLeuGluGlyArgTyrLysTrp 205  
 DB 560 NTAGAAAAAGTC-CACCTTCGATATTGNCATATGACCAACCGCTTGAAGGTCGCTCCAGTGG 618  
 QY 206 AspArgLeu 208  
 DB 619 GATCGACTT 627

RESULT 4

CNS0A6EV  
 LOCUS CNS0A6EV 736 bp mRNA linear HTC 06-FEB-2004  
 DEFINITION Arabidopsis thaliana Full-length cDNA Complete sequence from clone  
 GSLRS1872B03 of Silique of strain col-0 of Arabidopsis thaliana  
 (thale cress).  
 ACCESSION BX826140  
 VERSION BX826140.1 GI:42465305  
 KEYWORDS HTC; GSLT cDNA.  
 SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE 1 (bases 1 to 736)  
AUTHORS Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C., Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V., Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.  
TITLE Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:  
A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation

JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 736)  
AUTHORS Direct Submission  
TITLE Genoscope.  
JOURNAL Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

COMMENT The sequences are based on single pass reads.  
Life Technologies (a division of Invitrogen) members carried out full-length libraries construction : Temple G.  
Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.  
URGV INRA : Clepet C., Caboche M.  
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.  
http://www.genoscope.cns.fr/externe/sequences/Banque\_Projet\_EF/Full\_length  
http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.

FEATURES  
source Location/Qualifiers  
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/tissue\_type="Silique"  
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complement(1..736)  
/gene="At3g19150"

gene

ORIGIN  
Alignment Scores:  
Pred. No.: 4,35e-85 Length: 736  
Score: 900.00 Matches: 186  
Percent Similarity: 96.88% Conservative: 0  
Best Local Similarity: 96.88% Mismatches: 2  
Query Match: 86.12% Indels: 4  
DB: 3 Gaps: 1

US-09-980-758a-8 (1-209) x CNS0A6EV (1-736)

QY 6 LysAsnProArgGluLysMetSerGluArgLysArgGluLeuAlaGluAlaSer 25  
Db 2 AAAAATCAAGAGAGAAAAAATGACGAGAGAAAGCGAGAGCTTCGAGAGAAGCTTCA 61

QY 26 SerThrSerPheSerProLeuLysLysThrLysLeuAsnAspSerSerAspSerPro 45  
Db 62 AGCACAAGCTTCTCACCACTGAAGAAAAACGAGCTTAATGATCTCTCGATTCATCCG 121

QY 46 AspSerHisAspValIleValPheAlaValSerSerSerValAlaSerSerAlaAla 65  
Db 122 GACTCTCATGACGTATGCTTCGCGGTTCATCTTCTCGTTGCTTCGTGCGGCGCT 181

QY 66 LeuAlaSerAspGluCysSerValThrIleGlyGlyGluGluSerAspGlnSerSerSer 85  
Db 182 TTAGCGTCTGATGAATGTTCCGTTACCATCGGTGAGAAAGATGATCAGTCTCGAGT 241

QY 86 IleSerSerGlyCysPheThrSerGluSerLysGluIleAlaLysAsnSerSerPhe 105  
Db 242 ATCAGCTCCGGTGTGTTTACCAGTGAATCGAAAGAAATCGCGAAGAACAGTTCGTCGTTT 301

QY 106 GlyValAspLeuGluAspHisGlnIleGluThrGluThrGluThrSerThrPheIleThr 125  
Db 302 GGTGTAGATCTGGAGGATCATCAATCGAAACCGAAACCTCAACATTCATCACC 361

QY 126 SerAsnPheArgLysGluThrSerProValSerGluGlyLeuGlyGluThrThrGlu 145  
Db 362 AGCAATTTTCAGAAAGAGACGAGTCCAGTGGAGTGGGGTGGGAGAAACACACAGAA 421

QY 146 MetGluSerSerAlaThrLysArgLysGlnProGlyValArgLysThrProThrAla 165  
Db 422 ATGGAATCATCTCGCAACGAGAGAAACACCGGGGTGAGAGAGACTCCACGCGG 481

QY 166 AlaGluIleGluAspLeuPheSerGluLeuGluSerProAspLysLysLysGlnPhe 185  
Db 482 GCGGAGATTGAGGATTGTTCTCGAGCTAGAGAGTCAAGACGATTAAGAGAACCAATTC 541

QY 186 IleGluLys-----TyrAsnPheAspIle 193  
Db 542 ATAGAAAAGTGAGTCCATTTTACAAATTTTCATCATC 577

RESULT 5  
CNS0A66Q 784 bp mRNA linear HTC 06-FEB-2004  
LOCUS Arabidopsis thaliana Full-length cDNA Complete sequence from Clone  
DEFINITION GSLTSL148ZH01 of Silique of strain col-0 of Arabidopsis thaliana  
(thale cress).  
ACCESSION BX825610  
VERSION 1 GI:42464726  
KEYWORDS HIC; GSLT cDNA.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
REFERENCE 1 (bases 1 to 784)  
AUTHORS Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C., Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V., Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.  
TITLE Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:  
A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation

JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 784)  
AUTHORS Direct Submission  
TITLE Genoscope.  
JOURNAL Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

COMMENT The sequences are based on single pass reads.  
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Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.  
URGV INRA : Clepet C., Caboche M.  
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.  
http://www.genoscope.cns.fr/externe/sequences/Banque\_Projet\_EF/Full\_length  
http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.

FEATURES  
source Location/Qualifiers  
1..784  
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/clone="GSLTSL148ZH01"  
/tissue\_type="Silique"  
/plasmid="pCMVSPORT 6"  
complement(1..784)  
/gene="At3g19150"

gene

Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences  
A Combined Approach to Evaluate and Improve Arabidopsis Genome

**TITLE**  
Annotation  
Unpublished (2004)  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
The sequences are based on single pass reads.  
Life Technologies (a division of Invitrogen) members carried out full-length libraries construction : Temple G.  
Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.  
URGV INRA : Clepet C., Caboche M.  
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences).  
http://www.genoscope.cns.fr/externe/sequences/Banque\_Projet\_EF/EST  
http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.

**JOURNAL**  
**COMMENT**

**Alignment Scores:**  
Pred. No.: 2.73e-82 Length: 784  
Score: 874.00 Matches: 192  
Percent Similarity: 94.74% Conservative: 6  
Best Local Similarity: 91.84% Mismatches: 5  
Query Match: 83.64% Indels: 6  
DB: 3 Gaps: 0

US-09-980-758A-8 (1-209) x CNS0A66Q (1-784)

**QY** 6 LysAenProArgGluLysMetSerGluArgLysArgGluLeuAlaGluLysSer 25  
**Db** 2 AAAAAATCCAGAGAGAAAAAATGACGAGATAAAGCGAGAGCTTGCAGAGAAAGCTTCA 61  
**QY** 26 SerThrSerPheSerProLeuLysLysThrLysLeuAenAspSerSerAspSerPro 45  
**Db** 62 AGCAGAGCTTCTCACCACTGAAGAAACGAGCTTAATGATTTCTTGATTCATCACCG 121  
**QY** 46 AspSerHisAspValIleValPheAlaVal-SerSerSerValAlaSerSerAlaAl 65  
**Db** 122 GACTCTCATACGTATCGTCTTCGCGGTTTTCATCTTCTCCGTTCTGTCGCGGC 181  
**QY** 65 aleuAlaSerAspGluCysSerValThrIleGlyGlyGluGluSerAspGlnSerSerSe 85  
**Db** 182 TTTAGCATCTGATGAATGTTCCGTTTACCATTCCGTTGGAGAGAAAGTGATCAGTCTCGAG 241  
**QY** 85 rleSerSer-GlyCysPheThr-SerGluSerLysGluIleAlaLysAenSerSer 104  
**Db** 242 TATCAGCTCGCGGTTGTTTCCAGGAGTAAATCGAAAGAAATCCGGAAGATCAGTTCGTGC 301  
**QY** 105 PheGlyValAspLeuGluAspHisGlnIleGluThrGluThrGluThr-SerThrPheIl 124  
**Db** 302 TTTGGTGTAGATCTGGAGATCATCAATCGAACCGAAACCGAAGCCTCAACATTCAT 361  
**QY** 124 eThrSerAenPheArgLysGluThrSerProValSerGluGlyLeuGlyGluThrTh 144  
**Db** 362 CACCAGCAATTTTCAGAAAAGAGACAGTCCAGTCCAGTGGAGGTTTGGAGAAACCAAC 421  
**QY** 144 rGluMetGlu-SerSerSerAla-ThrLysArgLysGlnProGlyValArgLysThrPro 163  
**Db** 422 AGAATATGGAATGCATCATCGCCCAACGAGAGAGAAACACCGGGGGTGAGGAATACTCCA 481  
**QY** 164 ThrAlaAlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAspLysLys 183  
**Db** 482 ACGGCGCGGAGATTGAGAAATTTGTTCTCGAGCTTAAGAGTCAAGCAGTAAGAGAG 541  
**QY** 184 GlnPheIleGluLysTyraPheAspIleValAenAspGluProLeuGluGlyArgTyr 203  
**Db** 542 CAATTATGAGAAAGTACAACTTCGATATTGTCATATGACGAAACCGCTTAAAGGTCCCTAC 601  
**QY** 204 LysTrpAspArgLeu 208  
**Db** 602 AAGTCGGATCGACTT 616

**RESULT 6**  
**EX840619**  
**LOCUS**  
**DEFINITION**  
BX840619 Arabidopsis thaliana Silique Col-0 Arabidopsis thaliana  
cDNA clone GSLTSL172H03 5PRIM, mRNA sequence.  
**ACCESSION**  
BX840619  
**VERSION**  
BX840619.1 GI:42534702  
**KEYWORDS**  
EST.  
**SOURCE**  
Arabidopsis thaliana (thale cress)  
**ORGANISM**  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 457)  
Castelli V., Aury J.M., Jaillon O., Wincker P., Clepet C.,  
Menard M., Cruaud C., Quetier F., Scarpelli C., Schachter V.,  
Temple G., Caboche M., Weissenbach J. and Salanoubat M.

**REFERENCE**  
**AUTHORS**

**ORIGIN**

**Alignment Scores:**  
Pred. No.: 4.1e-42 Length: 457  
Score: 492.50 Matches: 120  
Percent Similarity: 84.77% Conservative: 8  
Best Local Similarity: 79.47% Mismatches: 17  
Query Match: 47.13% Indels: 9  
DB: 5 Gaps: 2

US-09-980-758A-8 (1-209) x BX840619 (1-457)

**QY** 11 LysLysMetSerGluArgLysArgGluLeuAlaGluLysSerThrSerPheSer 30  
**Db** 2 AAAAAATGAGCGAGAGAAAGCGAGAGTT-GCAGAGAAAGCTTCAAGCAAGCTTCTCA 60  
**QY** 31 ProLeuLysLysThrLysLeuAenAspSerSerAspSerProAspSerHisAspVal 50  
**Db** 61 CCACCTGAAGAAACCGAAGCTTAATGATTTCTGATTCATCACCAGACTCTCATGACGTC 120  
**QY** 51 IleValPheAlaValSerSerSerValAlaSerSerAlaAlaLeuAlaSerAspGlu 70  
**Db** 121 ATCGTCTTCGCGGTTTCATCTTCTCCGTTCTGTCGCGGCTTTAGCGTCTGATGAA 180  
**QY** 71 CysSerValThrIleGlyGlyGluGluSerAspGlnSerSerSerIleSerSerGlyCys 90  
**Db** 181 TGTTCGGTTTACCATTCCGTCGAGAGAAAGTATCAGTCTCCAGTATCAGCTCCGGTTGT 240  
**QY** 91 PheThrSerGluSerLysGluIleAlaLysAenSerSerPheGlyValAspLeuGlu 110  
**Db** 241 TTCACCGAGTGAATCGAAAGAAATCCGAGAAACAGTTCGTGTTATGTTAGTATCTCGA 300  
**QY** 110 uAspHisGlnIleGluThrGluThrSerThrPheIleThr-----SerAsnPh 128  
**Db** 301 GGATCATATAAATCAAAACCGAAAGAAAG-ACTACACATTCACACACCAGCGAACTTT 359  
**QY** 128 eArgLysGluThrSerProValSerGlu-----GlyLeuGlyGluThrThrGlu 145  
**Db** 360 CAGAAAAGAGACAGAGATT-CCAAGTGTAGTGGGATAGGATGAACACGACACACGAA 418  
**QY** 145 uMetGluSerSerSerAlaThrLysArgLys 155  
**Db** 419 ATGCGAACTCACTTATTCAGGCAACAGAAAG 449

**FEATURES**  
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/ecotype="Col-0"  
/db\_xref="taxon:3702"  
/clone="GSLTSL172H03"  
/tissue\_type="Silique"  
/clone\_lib="Arabidopsis thaliana Silique Col-0"

**ORIGIN**

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RESULT 7
AU228889/c
LOCUS AU228889 425 bp mRNA linear EST 23-APR-2002
DEFINITION AU228889 RAFL16 Arabidopsis thaliana cDNA clone RAFL16-57-G19 3',
mRNA sequence.
ACCESSION AU228889
VERSION AU228889.1 GI:19743536
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 425)
AUTHORS Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,
Akiyama, K., Enju, A., Ono, Y., Sakurai, T., Carninci, P., Kawai, J.,
Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shinagawa, A.,
Muramatsu, M., Hayashizaki, Y. and Shinozaki, K.
TITLE Large scale analysis of Arabidopsis full-length cDNA
JOURNAL Unpublished (2002)
COMMENT Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@tc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998) cDNA cleaved with BamHI
and XhoI was ligated to modified lambda FLC-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified pBluescript vector. Please visit our web
site (http://www.gsc.riken.go.jp/e/plant/index\_e.html) for further
details.
FEATURES             Location/Qualifiers
     source
     1..425
     /organism="Arabidopsis thaliana"
     /mol_type="mRNA"
     /db_xref="taxon:3702"
     /clone="RAFL16-57-G19"
     /lab_host="DH10B"
     /clone_lib="RAFL16"
     /note="Site_1: BamHI; Site_2: SalI; dark-grown"
ORIGIN
Alignment Scores:
Pred. No.: 1,278-28 Length: 425
Score: 365.00 Matches: 76
Percent Similarity: 95.06% Conservative: 1
Best Local Similarity: 93.83% Mismatches: 2
Query Match: 34.93% Indels: 2
DB: 1 Gaps: 0
US-09-980-758A-8 (1-209) x AU228889 (1-425)
Qy 130 LysGluThrSerProValSerGluGlyLeuGlyGluThrThrGluMetGluSerSer 149
Db 424 AAAGAGACGAGTCCATTGCTGAGTGGAGTGGAGAAACGACACAGAAATGGAATCATCA 365
Qy 150 SerAlaThrLysArgLysGlnProGlyValArgLysThrProThrAla-AlaGluIleGl 169
Db 364 TCGGCAACGACGAGAGAAAACACCGGGGTGAGGAAGACTCCAAACGGCGGGAGATTGA 305
Qy 169 uAspLeuPheSerGluLeuGluSerProAspAspLysLysGlnPheIleGluLysTy 189
Db 304 GGAATTGTTCGGAGCTAGAGAGTCAAGACGATGAAGAGCAATTCATAGAAAAGTA 245
Qy 189 rAsnPheAspIleValAsnAspGluProLeuGluGlyArgTyLys-TripAspArgLeu 208
Db 244 CAACCTTCGATATTGTCAATGACGAACCGCTTGAAGGTCCTTACAGAGTGGGATCGACTT 186
RESULT 8
BZ426940
LOCUS BZ426940 654 bp DNA linear GSS 13-DEC-2002
DEFINITION BONIN07TR BO 1.6 2 KB tot Brassica oleracea genomic clone BONIN07,
genomic survey sequence.
ACCESSION BZ426940
VERSION BZ426940.1 GI:26668452
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 654)
AUTHORS Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other GSSs: BONIN07TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
FEATURES             Location/Qualifiers
     source
     1..654
     /organism="Brassica oleracea"
     /mol_type="genomic DNA"
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     /db_xref="taxon:3712"
     /clone="BONIN07"
     /clone_lib="BO 1.6 2 KB tot"
     /note="Vector: pHOSt; Site 1: BstXI; 1.6-2 kb sheared
total DNA inserted into pHOSt using BstXI linkers"
ORIGIN
Alignment Scores:
Pred. No.: 4,2e-22 Length: 654
Score: 306.00 Matches: 91
Percent Similarity: 50.45% Conservative: 20
Best Local Similarity: 41.36% Mismatches: 51
Query Match: 29.28% Indels: 58
DB: 8 Gaps: 9
US-09-980-758A-8 (1-209) x BZ426940 (1-654)
Qy 13 MetSerGluArg-----LysArgGluLeu---AlaGluGluAlaSerSerThr 27
Db 6 ATGAGCGAGAGAGATCTCTAACTGCAAGCGTGTATCGCGAGCGCTTGAAGCTCCGAGCGCA 65
Qy 28 SerPheSerProLeuLysThrLysLeuAsnAspSerSerAspSerSerProAspSer 47
Db 66 AGCGACTCGCAACTCAAGAGAGAGAGCTCGATAT-----GACTCT 107
Qy 48 HisAspValIleValPheAlaValSerSerSerValAlaSerSerAlaAlaLeuAla 67
Db 108 CATGCGGTGGTCTTCTCGCGGTTCTCTTCTCTCCGTGGCTTCATCGATGATTCCTCT 167
Qy 68 SerAspGluCysSerValThrIleGlyGlyGluSerAspGlnSerSerSerIleSer 87
Db 168 CGAGCGCGGATCTCTGTATTACCTCCGCGGAGAGACGATGACAGAGTCCGATCATC--- 224
Qy 88 SerGlyCysPheThrSerGluSerLysGluIleAlaLysAsnSerSerPheGlyVal 107
Db 225 -----TGTTTCAGCAGTGAATCGAACGAAATCCGAGGAGAGTCCGACTGTTCTGTA 278
Qy 108 AspLeuGlu----- 110
Db 279 GATCTGGAGGTGAGATTTTTCGAAAAATCAGAAAGCTCGTCTCTGTTTGAACAATCATTCG 338
Qy 111 -----AspHis 112
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FEATURES
  source
    Location/Qualifiers
      1..700
        /organism="Brassica oleracea"
        /mol_type="genomic DNA"
        /db_xref="taxon:3712"
        /clone_lib="B.oleracea002"
        /note="Vector: pOTw13; Whole genome shotgun library from
        flowering buds. DNA was purified from a crude nuclear
        prep using Brassica oleracea TO1000DH3 buds provided by
        Thomas Osborn at the University of Wisconsin. Genomic
        DNA was provided by Pablo Rabinowicz (CSHL) and the
        shotgun library prepared at Washington University Genome
        Sequencing Center."
ORIGIN
Alignment Scores:
Pred. No.:      2,896-21      Length:      700
Score:          298.50      Matches:      88
Percent Similarity: 49.11%      Conservative: 22
Best Local Similarity: 39.29%      Mismatches:  51
Query Match:    28.56%      Indels:      63
DB:             8          Gaps:        9
US-09-980-758A-8 (1-209) x BZ083701 (1-700)
Qy  17 LysArgGluLeuAlaGlu---GluAlaSerSerThrSerPheSerProLeuLysLysThr 35
Db  44 AAGCGTACTACAGAAAGCTTGAGCTCGAGCGCAAGCACTCGCAACTCAGAGAGAG 103
Qy  36 LysLeuAsnAspSerSerAspSerSerProAspSerHisAspValIleValPheAlaVal 55
Db  104 AAGTCGATGAT-----GACTCTCATGGCGTGGTCTCTCTCGCGGT 145
Qy  56 SerSerSerSerValAlaSerSerAlaAlaLeuAlaSerAspGluCysSerValThrIle 75
Db  146 CTTTCTCCTTCGTTGGCTTCATCGGATGATTCCTCGAGCGGATGCTCTGTACCTCC 205
Qy  76 GlyGlyGluGluSerAspGlnSerSerIleSerSerGlyCysPheThrSerGluSer 95
Db  206 GCCGAGAGACGATGACAGAGCTCGATCATC-----TGTTTCAGAGTGAATCG 256
Qy  96 LysGluIleAlaLysAsnSerSerSerPheGlyValAspLeuGlu-----110
Db  257 AACGAAATCCCGAGGAGAGTCCGACTGTTTCTGTAGATCTGGAGGTGAGATTTTCGAA 316
Qy  110 -----TCTCACAGAAACGAGGCGAATCCAGCGAGTGAAGCTTTGGGA 490
Db  317 AATCAGAGCTGCTCTGTTTGAACAATCATTCGATGACTCAAAATCTGGAATCTTCA 376
Qy  111 -----AspHisGlnIleGluThrGluThrGluThr 120
Db  377 TTGATTTCTTTTCGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 436
Qy  121 SerThrPheIleThrSerAsnPheArgLysGluThrSerProValSerGluLysGly 140
Db  437 TCTGGCGCATC-----TCTCACAGAAACGAGGCGAATCCAGCGAGTGAAGCTTTGGGA 490
Qy  141 GluThrThrThrGluMetGluSerSerSerAlaThrLysArg-----LysGln 156
Db  491 GAG---ACACAGAGTTTGGAAATCATCATCGCGGTGAGAGAGGGATGATCGGAAAGTTCA 547
Qy  157 ProGlyValArgLysThrProThrAlaAlaGluIleGluAspLeuPheSerGluLeuGlu 176
Db  548 CCGNAGTGACCAAGAAATCCGACGCCGCGGAGATTGAGGATCTTTATCGAGCTAGAG 607
Qy  177 SerProAspAspLysLysGlnPheIleGluLys-----188
Db  608 AATAAGAT-----CAGAAGCGTTTCATGGATAAGTCAGTCTCATCTCCGATCTCTTCT 661
Qy  189 ---TyrAsnPhe 191
Db  662 TCCTTTAATTTT 673
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RESULT 11
LOCUS      AI728644
DEFINITION BNLGH111291 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar
            to (AJ0021173) cyclin-dependent kinase inhibitor protein
            [Chenopodium rubrum], mRNA sequence.
ACCESSION  AI728644
VERSION     AI728644.1
KEYWORDS   GI:5047496
SOURCE     Gossypium hirsutum (upland cotton)
ORGANISM   Gossypium hirsutum
REFERENCE  1 (bases 1 to 646)
AUTHORS   Blewitt, M., Matz, E.C., Davy, D.F. and Burr, B.
TITLE     ESTs from developing cotton fiber
JOURNAL   Unpublished (1999)
COMMENT   Contact: Ben Burr
          Biology Department
          Brookhaven National Laboratory
          Upton, NY 11973 USA
          Tel: 516-344-3396
          Fax: 516-344-3407
          Email: burr@bnl.bnl.gov
          Seq primer: T3 Primer.
          Location/Qualifiers
            1..646
              /organism="Gossypium hirsutum"
              /mol_type="mRNA"
              /cultivar="Acala Maxxa"
              /db_xref="taxon:3635"
              /tissue_type="immature fiber"
              /dev_stage="Six days post anthesis"
              /lab_host="Xlri-Blue"
              /clone_lib="Six-day Cotton fiber"
              /note="Vector: pBluescript II KS+"
ORIGIN
Alignment Scores:
Pred. No.:      9,67e-16      Length:      646
Score:          246.00      Matches:      77
Percent Similarity: 50.48%      Conservative: 29
Best Local Similarity: 36.67%      Mismatches:  68
Query Match:    23.54%      Indels:      36
DB:             1          Gaps:        10
US-09-980-758A-8 (1-209) x AI728644 (1-646)
Qy  15 GluArgLysArgGluLeuAlaGlu---GluAlaSerSerThrSerPheSerProLeuLys 33
Db  60 AAACGAAGTCAGAGAGAGCTGAATGGAAGCTTCAGACAGAGCTTCTCATATCAAG 119
Qy  34 LysThrLys-----LeuAsnAspSerSerAspSerSerProAsp---46
Db  120 AGAAGAAAACACTGTTGGTTCTCGAGAAATTGAGATTTAGAGTTAACTTACCAGGACATT 179
Qy  47 -----SerHisaspValIleValPheAlaValSer 56
Db  180 GAGCTCGGAACCACTCGCATCCTTTTCGAAATTCGTGACAAAGCCTATTATTACTAGCTACT 239
Qy  57 SerSerSerValAlaSerSerAlaLeuAlaLeuAlaSerAspGluCysSerValThrIleGly 76
Db  240 TCCTCG-----GGTCTTGTGGAGTGCTTTCCGAGATATGTTGTCGGTCTCTTCTCC 293
Qy  77 GlyGluGluSerAspGlnSerSerSerIleSerSerGlyCysPheThrSerGluSerLys 96
Db  294 GGCAATTCATCG-----GCTTCTCGTTGTCGAGCAACGAGTCGTGT 335
Qy  97 GluIleAlaLysAsnSerSerPheGlyValAspLeuGluAspHisGlnIleGluThr 116
Db  336 GATATTCTCAAAGATAGCTTGAGATTCT---GTAGATCTAGAGCGGAGAGATTTTGAAGACT 392
```



JOURNAL  
COMMENT

Unpublished (2004)  
Contact: Joerg Bohlmann  
Genome BC forest genomics program  
University of British Columbia  
UBC Biotechnology Laboratory, 6174 University Boulevard, Rm. 237,  
Vancouver, British Columbia, Canada, V6T 1Z3  
Tel: 1-604-822-0282  
Fax: 1-604-822-6097  
Email: bohlmann@interchange.ubc.ca  
Plate: WS02516 row: J column: 17  
High quality sequence stop: 919  
POLYA=Yes.

## FEATURES

source

Location/Qualifiers  
1..919

/organism="Populus balsamifera subsp. trichocarpa"  
/mol\_type="mRNA"  
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/clone="WS02516\_J17"  
/sex="Male"  
/lab\_host="E. coli DH10B T1 phage resistant cells"  
/clone\_lib="PT-MB-N-A-15"  
/note="Vector: pBluescript II SK (+) XR; Site 1: EcoRI (5' end of cDNA); Site 2: XhoI (3' end of cDNA); Terminal vegetative buds from 20 year old trees harvested near Corvallis, Oregon on September 19th, 2001. cDNA was prepared from 5 micrograms of mRNA and directionally ligated into the pBluescript II SK (+) XR vector using the pBluescript II XR cDNA Library Construction Kit according to manufacturer's instructions with modifications (Stratagene). Plasmid DNA was then transformed by electroporation into DH10B cells (Invitrogen) for propagation. Normalization was applied according to published methods (Bonaldo M.F. et al. (1996) Genome Research 6(9):791) in order to reduce the abundance of highly expressed transcripts."

## ORIGIN

Alignment Scores:  
Pred. No.: 8,69e-15 Length: 919  
Score: 239.00 Matches: 76  
Percent Similarity: 55.87% Conservative: 43  
Best Local Similarity: 35.68% Mismatches: 65  
Query Match: 22.87% Indels: 29  
D: 7 Gaps: 12

US-09-980-758A-8 (1-209) x CV242992 (1-919)

Qy 6 LysAanProArgGluLys-LysMetSerGluArgLysArgGluLeuAlaGlu----- 22  
Db 913 AAGATGGGAGCGCGGAGGATAGTAAAGCA-----ATAGCTGAACCTGGAAAT 863  
Qy 23 ----GluAlaSerThrSerPheSerProLeuLysLysThrLysLeuAsnAspSerSe 41  
Db 862 TCTAGAACTTCAGTCACAGTTCTCT-----AAGAAATGAATTTGATTTTGACGA 809  
Qy 41 rAspSerPro-----AspSerHisAspValIleValPheAlaVa 55  
Db 808 GTTAGCTTACCTCGTTTAATTTCAAGCTCCAAGCTCAT-----CTTGCACCACTAT 755  
Qy 55 lSerSerSerValAlaSerSerAlaAlaLeuAlaSerAspGluCysSerValThrIl 75  
Db 754 GTCCCGGACAAATTTGATTTCTCGCGGCTTCATCGAAATTCGATCGCTTTATACC-- 697  
Qy 75 edgLyGluGluSerAspGlnSerSerSerIleSerSerGlyCysPheThrSerGluse 95  
Db 696 ----GGCAATTCAGCTGTGGCGACTCTCCGGTTTCTGC---TGCTCCAGCAATGAATC 644  
Qy 95 rlyGluLeuAlaLysAsnSerSerPheGlyValAspLeuGluAspHisGlnIleGl 115  
Db 643 GATCAAGGTTGTGAAGGACAGCTTGAGGTTT---ATAGATCTGGAGCGGAAG-----AG 593

Qy 115 uThrGluThrGluThrSerThrPheIleThrSerAsnPheArgLysGluThrSerProVa 135  
Db 592 TTCCGAACGAAAGCTCGACGTGCAATGACAGGAAATTCAGTAGAGACACCACTCTTC 533  
Qy 135 lSerGlu-----GlyLeuGlyGluThrThrGluMetGluSerSerAlaThrLy 153  
Db 532 AAGCGAGTTTCACGGGATGACTCGCGCGAGCGTGGAGAAAGAAAGAAATTCACAG 473  
Qy 153 sAtgLyGlnProGlyValArgLysThrProThrAlaAlaGluIleGluAspLeuPheSe 173  
Db 472 GAGAAAGTCCCGCTGTG---AAATGCCGAGTCAGGCTGAGATCGATCGTTTTCGC 416  
Qy 173 rGluLeuGluSerProAspLysLysLysGlnPheIleGluLysThrAsnPheAspIl 193  
Db 415 GGGGGCAGAGAGA-----GAGGAGCAGAAAGATTTGCAGAGAAGTACAACTACGATGT 362  
Qy 193 eValAsnAspGluProLeuGluGlyArgTyrLysTip 205  
Db 361 TGTGAAGGATTTGCCAGTGGAGGGTGCCTACCACTGG 325

## RESULT 14

CF212120

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1..888

/organism="Vitis vinifera"

/mol\_type="mRNA"

/cultivar="Cabernet Sauvignon"

/db\_xref="taxon:29760"

/clones="CAST0004\_IIF\_A05"

/sex="Hermaphrodite"

/dev\_stage="Pre-bloom (10-11 days before bloom)"

/lab\_host="DHSalpa"

/clone\_lib="Vitis vinifera cv. cabernet sauvignon Stem -"

CAST"

/note="Organ: Stem; Vector: pNDR; Site 1: sfiI; Site 2: sfiI; CAST is a cDNA library of Vitis vinifera cv. 'Cabernet Sauvignon' stems. Samples were collected May 13, 2002 from pre-bloom plants (10-11 days before bloom), pre-veraison. Sampled vines were located at the University of California, Davis, Experimental Vineyard. cDNAs were made by oligo-dT priming and directionally cloned. 5' and 3' adaptors were used in cloning as follows: 5'-AAGCAGTGTGATCAACGAGATGCCATACGCGCGG-3' and 5'-ATTCTAGGCGCGGCGGCATG-dt(30)NN-3'. Library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-3 kb size fraction."

## ORIGIN





```
||||| :||| ||| ||||| :||| |||
230 TGTTCAC--AGTCTGGCTTAGAATTATCTGATCATGCTGTGTTTCGACTTCATGTTGC 286
Qy 91 PheThrSerGluSerLysGluIleAlaLysAsnSerSerPheGlyValAspLeuGlu 110
Db 287 TCCAGTCCACAGATCCAGTGAGAGATAGAA-----TTTGTAGATCTGAAG 331
Qy 111 AspHisGlnIleGluThrGluThrGluThrSerThrPhe----- 123
Db 332 GATGAGAGTGTGATGTGGAGCTGAACATCGACGTATTATGGATGCAGAGAAAGGAGA 391
Qy 124 -----IleThrSerAsnPheArgLysGluThrSerProValSerGluGlyLeuGly 140
Db 392 GACGCGACGCTGTCCAGCGAGCTTGAAACTGAAGCTGGAGAGAATCAGACGGCTG--- 448
Qy 141 GluThrThrThrGluMetGluSerSerSerAlaThrLysArgLysGlnProGlyValArg 160
Db 449 ---GATTCAACTGGAGAGCCATCATCAGAGGCAAACTCTCGCCGTAGATCAACCGTGGAG 505
Qy 161 LysThrProThrAlaAlaGluIleGluAspLeuPheSerGluLeuGluSerProAspAsp 180
Db 506 AGCATGCTGCCAAGCTCTGAATTTGAGGACTTCTTCGCTGAGCTGAG----- 553
Qy 181 LysLys-----LysGlnPheIleGluLysTyrAsnPheAspIleValAsnAspGluPro 198
Db 554 AAAAAGCTCGTAAACAAATTTTCTCAGAAAGTATAACTTCGACTTCGTGAAAGAGAGGCCA 613
Qy 199 LeuGluGlyArgTyrLysTyr 205
Db 614 ATGGAAGGACGTTACAAGTGG 634
```

Search completed: September 30, 2005, 13:54:39  
Job time : 3174 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 30, 2005, 09:14:02 ; Search time 81 Seconds  
(without alignments)  
997.937 Million cell updates/sec

Title: US-09-980-758A-8  
Perfect score: 1045  
Sequence: 1 PDLPLKPNREKMSRKREL.....NFDIYNDEPLEGRYKWDRLX 209

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1044	99.9	208	4	AAB47001 Plant D-1
2	1007	96.4	212	3	AAY44337 Arabidops
3	1007	96.4	212	5	AAS25103 Arabidops
4	969	92.7	196	5	AAS25104 Arabidops
5	351.5	33.6	207	3	AAY44338 Arabidops
6	351.5	33.6	207	5	AAS25105 Arabidops
7	346.5	33.2	195	5	AAS25106 Arabidops
8	184	17.6	206	4	AAB47004 Plant D-1
9	177	16.9	209	2	AAS98179 Arabidops
10	177	16.9	209	3	AAG17611 Arabidops
11	177	16.9	209	3	AAG38486 Arabidops
12	177	16.9	209	5	AAS25110 Arabidops
13	177	16.9	209	8	ADN72203 Thale cre
14	175.5	16.8	191	3	AAY44335 Arabidops
15	175.5	16.8	191	3	AAG15426 Arabidops
16	175.5	16.8	191	3	AAG42858 Arabidops
17	175.5	16.8	191	5	AAS25101 Arabidops
18	174	16.7	171	3	AAG42859 Arabidops
19	174	16.7	171	3	AAG15427 Arabidops
20	172	16.5	205	3	AAPO1952 Cyclin de
21	172	16.5	205	3	AAB27254 Soybean c
22	168.5	16.1	196	3	AAB27259 Chenopodi
23	168.5	16.1	196	3	AAY44340 Chenopodi
24	168.5	16.1	196	5	AAS25108 Chenopodi
25	162.5	15.6	256	3	AAG40486 Arabidops

26	162.5	15.6	289	3	AAB27262 Arabidops
27	162.5	15.6	289	3	AAG40485 Arabidops
28	162.5	15.6	289	5	AAS25109 Arabidops
29	162.5	15.6	289	5	AAY72581 Arabidops
30	162.5	15.6	289	8	ADN72347 Thale cre
31	159	15.2	176	3	AAY44336 Arabidops
32	159	15.2	176	5	AAS25102 Arabidops
33	159	15.2	183	3	AAG38487 Arabidops
34	159	15.2	183	3	AAG17612 Arabidops
35	155	14.8	222	5	AAS25111 Arabidops
36	154.5	14.8	201	3	AAG40487 Arabidops
37	153	14.6	262	5	ABG65670 OsiCK 2 p
38	152	14.5	216	2	AAW98180 Arabidops
39	152	14.5	222	8	ADN72351 Thale cre
40	150.5	14.4	137	5	AAS25107 Arabidops
41	149	14.3	194	5	ABG65691 Rice OsiC
42	147.5	14.1	190	3	AAB27258 Wheat cyc
43	144.5	13.8	136	3	AAY44339 Arabidops
44	139	13.3	419	8	ADR86387 Aspergill
45	139	13.3	446	8	ADR86528 Aspergill

ALIGNMENTS

RESULT 1  
AAB47001  
ID AAB47001 standard; protein; 208 AA.  
XX  
AC AAB47001;  
XX  
DT 22-MAR-2001 (first entry)  
XX  
DE Plant D-like cyclin inhibitor BRO4.  
XX  
KW Plant; D-like cyclin inhibitor gene; BRO4; hyperplastic; variant;  
KW growth rate; dividing cells; inactivation; protoplast; seed; root cell;  
KW meristem; leaf.  
XX  
OS Arabidopsis thaliana.  
XX  
FH Key Location/Qualifiers  
FT Protein 13..208  
FT /label= BRO4  
XX  
PN WO200069883-A1.  
XX  
PD 23-NOV-2000.  
XX  
PF 15-MAY-2000; 2000WO-US013379.  
XX  
PR 14-MAY-1999; 99US-0134373P.  
XX  
PA (HUTC-) HUTCHINSON CANCER RES CENT FRED.  
XX  
PI Roberts J, Kelly B;  
XX  
DR WPI; 2001-024998/03.  
XX  
N-PSDB; AAC85201.  
XX  
PT Functionally inactivating expression of plant D-like cyclin inhibitor  
PT gene for producing a hyperplastic variant plant, modulating the growth  
PT and/or yield of plants, and increasing the proportion of dividing cells.  
XX  
PS Claim 15; Page 41-42; 50pp; English.  
XX  
CC The sequence given in AAB47001 represents a plant D-like cyclin  
CC inhibitor, BRO4. The DNA encoding this sequence may be used to produce a  
CC hyperplastic variant plant, increase the growth rate of a plant, or  
CC increase the proportion of dividing cells in a plant cell population,  
CC relative to a wild-type plant, by functionally inactivating the  
CC expression of a plant D-like cyclin inhibitor gene in a plant. The DNA  
CC sequence is homologous to a sequence present in a D-like cyclin inhibitor



CC inhibitor polypeptide (such as ICK1, ICK2, ICN2, ICN6, ICN7, ICN8 and  
CC ICDK), a cyclin polypeptide, a CDK, or a polypeptide that modulates the  
CC degradation of a CDK inhibitor polypeptide. The method is useful for  
CC modifying the growth and development of plants e.g. morphogenesis,  
CC growth, multiplication, enlargement, differentiation or maturation of a  
CC cell or plant. It is particularly useful in plant breeding. The present  
CC sequence is A. thaliana ICN2 protein  
XX  
SQ Sequence 212 AA;

Query Match 96.4%; Score 1007; DB 5; Length 212;  
Best Local Similarity 99.5%; Pred. No. 4.4e-78;  
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 KNPREKMSRKRELAEEASSTFSPLKTKLNDSSDSDSHDVIVFAVSSSVASSAA 65  
DB 10 KNPREKMSRKRELAEEASSTFSPLKTKLNDSSDSDSHDVIVFAVSSSVASSAA 69  
QY 66 LASDECSVTIGGESDQSSISGCGFTSSKETAKNSSFGVDLEDHQIETETSTFIT 125  
DB 70 LASDECSVTIGGESDQSSISGCGFTSSKETAKNSSFGVDLEDHQIETETSTFIT 129  
QY 126 SNFRKETSPVSEGLGTTTTEMESSATKKRQPGVRKTPPTAAEIEDLFSELESDDKKQF 185  
DB 130 SNFRKETSPVSEGLGTTTTEMESSATKKRQPGVRKTPPTAAEIEDLFSELESDDKKQF 189  
QY 186 IEKYNFDVNDPELEGRYKWDRL 208  
DB 190 IEKYNFDVNDPELEGRYKWDRL 212

RESULT 4  
AAE25104  
ID AAE25104 standard; protein; 196 AA.  
XX AC AAE25104;  
XX DT 30-OCT-2002 (first entry)  
XX DE Arabidopsis thaliana ICN2 protein #2.  
XX KW Plant development; cyclin-dependent kinase; CDK inhibitor; ICK1; ICK2;  
KW ICN2; ICN6; ICN7; ICN8; ICDK; morphogenesis; maturation; enlargement;  
KW plant breeding; growth.  
XX OS Arabidopsis thaliana.  
XX PN WO200250292-A2.  
XX PD 27-JUN-2002.  
XX PF 18-DEC-2001; 2001WO-CA001825.  
XX PR 18-DEC-2000; 2000US-0255908P.  
XX PA (MIAC ) CANADA MIN AGRIC & AGRI-FOOD CANADA.  
XX PA (UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.  
XX PI Wang H, Zhou Y, Fowke LC;  
XX DR WPI; 2002-519888/55.  
XX DR N-PSDB; AAD40765.  
XX PT Modifying plant development, e.g. growth or maturation, which is  
PT particularly useful in plant breeding, by introducing nucleic acids  
PT coding for cyclin-dependent kinase (CDK) inhibitor, cyclin or proteins  
PT that bind to CDK inhibitors.  
XX PS Disclosure; Fig 8B; 89pp; English.  
XX CC The invention relates to a method for the development of a plant. The  
CC method involves introducing into a plant cell a nucleic acid encoding a  
CC protein that binds or interacts with a cyclin-dependent kinase (CDK)

CC inhibitor polypeptide (such as ICK1, ICK2, ICN2, ICN6, ICN7, ICN8 and  
CC ICDK), a cyclin polypeptide, a CDK, or a polypeptide that modulates the  
CC degradation of a CDK inhibitor polypeptide. The method is useful for  
CC modifying the growth and development of plants e.g. morphogenesis,  
CC growth, multiplication, enlargement, differentiation or maturation of a  
CC cell or plant. It is particularly useful in plant breeding. The present  
CC sequence is A. thaliana ICN2 protein  
XX  
SQ Sequence 196 AA;

Query Match 92.7%; Score 969; DB 5; Length 196;  
Best Local Similarity 99.5%; Pred. No. 7.1e-75;  
Matches 195; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 MSERKRELAEEASSTFSPLKTKLNDSSDSDSHDVIVFAVSSSVASSAALASDECS 72  
DB 1 MSERKRELAEEASSTFSPLKTKLNDSSDSDSHDVIVFAVSSSVASSAALASDECS 60  
QY 73 VTIGGESDQSSISGCGFTSSKETAKNSSFGVDLEDHQIETETSTFITSNFRKET 132  
DB 61 VTIGGESDQSSISGCGFTSSKETAKNSSFGVDLEDHQIETETSTFITSNFRKET 120  
QY 133 SPVSEGLGTTTTEMESSATKKRQPGVRKTPPTAAEIEDLFSELESDDKKQFIEKYNFD 192  
DB 121 SPVSEGLGTTTTEMESSATKKRQPGVRKTPPTAAEIEDLFSELESDDKKQFIEKYNFD 180  
QY 193 IVNDEPLEGRYKWDRL 208  
DB 181 IVNDEPLEGRYKWDRL 196

RESULT 5  
AAY44338  
ID AAY44338 standard; protein; 207 AA.  
XX AC AAY44338;  
XX DT 29-FEB-2000 (first entry)  
XX DE Arabidopsis thaliana CDK inhibitor, ICN6.  
XX KW Cyclin-Dependent Kinase inhibitor; CDK; Interactor of Cyclin 6; ICN6;  
KW Cdc2a; D-Class cyclin; CycD1; CycD2; CycD3; morphogenesis;  
KW antisense construct; tissue-specific promoter; transgenic plant;  
KW male sterility.  
XX OS Unidentified.  
XX PN WO9964599-A1.  
XX PD 16-DEC-1999.  
XX PF 08-JUN-1999; 99WO-CA000532.  
XX PR 08-JUN-1998; 98CA-02235978.  
XX PR 31-DEC-1998; 98CA-02256121.  
XX PA (MIAC ) AGRIC & AGRI-FOOD CANADA.  
XX PA (UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.  
XX PA (CANA ) NAT RES COUNCIL CANADA.  
XX PI Wang H, Fowke LC, Crosby WL;  
XX DR WPI; 2000-097540/08.  
XX DR N-PSDB; AA229418.  
XX PT Modifying plant cell development using nucleic acid encoding inhibitor of  
PT cyclin-dependent kinase, or corresponding antisense sequence, e.g. for  
PT inducing male sterility.  
XX PS Disclosure; Fig 7; 58pp; English.  
XX CC The present protein sequence is ICN6, which inhibits A. thaliana Cyclin-

CC Dependent Kinase (CDK). Interactor of Cyclin 6 (ICN6) interacts with  
 CC Cdc2a, D-class cyclins, CycD1, CycD2 and CycD3 and shares functional  
 CC sequence similarity with ICN1. Growth, morphogenesis, multiplication,  
 CC enlargement, differentiation and maturation of plant cells can be  
 CC modified by transforming them with nucleic acid encoding CDK inhibitor or  
 CC antisense construct complementary to the inhibitor gene, operably linked  
 CC to a tissue-specific promoter. The transgenic plants exhibit alteration  
 CC of traits such as petals, male sterility and ability to set seeds  
 XX  
 XX Sequence 207 AA;

Query Match 33.6%; Score 351.5; DB 3; Length 207;  
 Best Local Similarity 44.5%; Pred. No. 6.3e-22;  
 Matches 93; Conservative 30; Mismatches 57; Indels 29; Gaps 10;  
 QY 9 REKKMSERKRLAEAEASSTSFPLKTKLNDSSD--SSPDSDHVDVFAVSSSSVASSAAL 66  
 DB 11 REMSETPKRDEYEGSN-----IKRWLDDDDVLRSPTR-----TLSSSSSSSLAYS 59  
 QY 67 ASDE---CSVTIGGESDQ-SSSISSGCGFTSESKEIAKNSSSFGVDLEDHQIETETST 122  
 DB 60 VSDSGGFCVALSEEDDHLSSISGCGSSSETNEIATRLPF--SDLEAHEI-SETEIST 116  
 QY 123 FITSNFRKETSVPVSEGLGET-----TTEMSSSATKPKQGVKXTPTAAIEDLFSELE 176  
 DB 117 LLTNFRKQGISSENELGETAEMDSATTEMRDQRKTEKKK-MEKSPTQABLDDFFSAE 175  
 QY 177 SPDDKKKQFIEKYNFDVNDPELEGYKW 205  
 DB 176 RYE--QKRFTKYNFDVNDPTLEGYQW 202

RESULT 6  
 AAE25105  
 ID AAE25105 standard; protein; 207 AA.  
 XX  
 AC AAE25105;  
 XX  
 DT 30-OCT-2002 (first entry)  
 XX  
 DE Arabidopsis thaliana ICN6 protein #1.  
 XX  
 KW Plant development; cyclin-dependent kinase; CDK inhibitor; ICN1; ICN2;  
 KW ICN2; ICN6; ICN7; ICN8; ICN8; ICN8; ICN8; ICN8; ICN8; ICN8; ICN8;  
 KW plant breeding; growth.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 PN WO200250292-A2.  
 XX  
 PD 27-JUN-2002.  
 XX  
 PF 18-DEC-2001; 2001WO-CA001825.  
 XX  
 PR 18-DEC-2000; 2000US-0255908P.  
 XX  
 PA (MIAC ) CANADA MIN AGRIC & AGRI-FOOD CANADA.  
 PA (UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.  
 XX  
 PI Wang H, Zhou Y, Fowke LC;  
 XX  
 DR WPI; 2002-519888/55.  
 DR N-PSDB; AAD40766.  
 XX  
 PT Modifying plant development, e.g. growth or maturation, which is  
 PT particularly useful in plant breeding, by introducing nucleic acids  
 PT coding for cyclin-dependent kinase (CDK) inhibitor, cyclin or proteins  
 PT that bind to CDK inhibitors.  
 XX  
 PS Disclosure; Fig 9A; 89pp; English.  
 XX  
 CC The invention relates to a method for the development of a plant. The  
 CC method involves introducing into a plant cell a nucleic acid encoding a

CC protein that binds or interacts with a cyclin-dependent kinase (CDK)  
 CC inhibitor polypeptide (such as ICN1, ICN2, ICN2, ICN6, ICN7, ICN8 and  
 CC ICN8), a cyclin polypeptide, a CDK, or a polypeptide that modulates the  
 CC degradation of a CDK inhibitor polypeptide. The method is useful for  
 CC modifying the growth and development of plants e.g. morphogenesis,  
 CC growth, multiplication, enlargement, differentiation or maturation of a  
 CC cell or plant. It is particularly useful in plant breeding. The present  
 CC sequence is A. thaliana ICN6 protein  
 XX  
 XX Sequence 207 AA;

Query Match 33.6%; Score 351.5; DB 5; Length 207;  
 Best Local Similarity 44.5%; Pred. No. 6.3e-22;  
 Matches 93; Conservative 30; Mismatches 57; Indels 29; Gaps 10;  
 QY 9 REKKMSERKRLAEAEASSTSFPLKTKLNDSSD--SSPDSDHVDVFAVSSSSVASSAAL 66  
 DB 11 REMSETPKRDEYEGSN-----IKRWLDDDDVLRSPTR-----TLSSSSSSSLAYS 59  
 QY 67 ASDE---CSVTIGGESDQ-SSSISSGCGFTSESKEIAKNSSSFGVDLEDHQIETETST 122  
 DB 60 VSDSGGFCVALSEEDDHLSSISGCGSSSETNEIATRLPF--SDLEAHEI-SETEIST 116  
 QY 123 FITSNFRKETSVPVSEGLGET-----TTEMSSSATKPKQGVKXTPTAAIEDLFSELE 176  
 DB 117 LLTNFRKQGISSENELGETAEMDSATTEMRDQRKTEKKK-MEKSPTQABLDDFFSAE 175  
 QY 177 SPDDKKKQFIEKYNFDVNDPELEGYKW 205  
 DB 176 RYE--QKRFTKYNFDVNDPTLEGYQW 202

RESULT 7  
 AAE25106  
 ID AAE25106 standard; protein; 195 AA.  
 XX  
 AC AAE25106;  
 XX  
 DT 30-OCT-2002 (first entry)  
 XX  
 DE Arabidopsis thaliana ICN6 protein #2.  
 XX  
 KW Plant development; cyclin-dependent kinase; CDK inhibitor; ICN1; ICN2;  
 KW ICN2; ICN6; ICN7; ICN8; ICN8; ICN8; ICN8; ICN8; ICN8; ICN8;  
 KW plant breeding; growth.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 PN WO200250292-A2.  
 XX  
 PD 27-JUN-2002.  
 XX  
 PF 18-DEC-2001; 2001WO-CA001825.  
 XX  
 PR 18-DEC-2000; 2000US-0255908P.  
 XX  
 PA (MIAC ) CANADA MIN AGRIC & AGRI-FOOD CANADA.  
 PA (UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.  
 XX  
 PI Wang H, Zhou Y, Fowke LC;  
 XX  
 DR WPI; 2002-519888/55.  
 DR N-PSDB; AAD40766.  
 XX  
 PT Modifying plant development, e.g. growth or maturation, which is  
 PT particularly useful in plant breeding, by introducing nucleic acids  
 PT coding for cyclin-dependent kinase (CDK) inhibitor, cyclin or proteins  
 PT that bind to CDK inhibitors.  
 XX  
 PS Disclosure; Fig 9B; 89pp; English.  
 XX  
 CC The invention relates to a method for the development of a plant. The  
 CC method involves introducing into a plant cell a nucleic acid encoding a

CC protein that binds or interacts with a cyclin-dependent kinase (CDK)  
CC inhibitor polypeptide (such as ICK1, ICK2, ICK6, ICK7, ICK8 and  
CC ICK9), a cyclin polypeptide, a CDK, or a polypeptide that modulates the  
CC degradation of a CDK inhibitor polypeptide. The method is useful for  
CC modifying the growth and development of plants e.g. morphogenesis,  
CC growth, multiplication, enlargement, differentiation or maturation of a  
CC cell or plant. It is particularly useful in plant breeding. The present  
CC sequence is A. thaliana ICK6 protein  
XX  
SQ Sequence 195 AA;  
Query Match 33.2%; Score 346.5; DB 5; Length 195;  
Best Local Similarity 45.4%; Pred. No. 1.6e-21;  
Matches 93; Conservative 27; Mismatches 58; Indels 27; Gaps 10;  
QY 13 MSERKRELAEEASTSFSPKTKTLNDSSD--SSPDSDHVDVFAVSSSVASSAALASDE 70  
DB 1 MSETKPKRDEYEG--SNIKRMRLDDDDVLRSPTR-----TLSSSSSSSLAYSVSDS 51  
QY 71 ---CSVTIGGERSDQ-SSSISSGCFTSSEKIAKNSSSFGVLEHQIETETSTFTS 126  
DB 52 GGFCSVALSEEDDHLSSISGSSSTNEIATRLPF--SDLEAHEI-SETEISTLTN 108  
QY 127 NFRKETSPPVSEGLGET-----TTEMSSSATKQKQGVKTKPTAAEIEDLSELESPPD 180  
DB 109 NFRKQIGISSENIGETAEMDSATTEMRDQKTEKKK-MEKSPTQAELODFFSAERYE- 166  
QY 181 KKQFIEKYNFDVNDPELEGRYKW 205  
DB 167 -QKRFTEKYNVDVNDTPLEGRYQW 190  
RESULT 8  
AAB47004  
ID AAB47004 standard; protein; 206 AA.  
XX  
AC AAB47004;  
XX  
XX 22-MAR-2001 (first entry)  
XX Plant D-like cyclin inhibitor BRO3.  
XX  
XX Plant; D-like cyclin inhibitor gene; BRO4; hyperplastic; variant;  
XX growth rate; dividing cells; inactivation; protoplast; seed; root cell;  
XX meristem; leaf.  
XX  
XX Arabidopsis thaliana.  
XX  
XX Key Location/Qualifiers  
XX Protein 20..202  
XX /label= BRO3  
XX  
XX WO200069883-A1.  
XX  
XX 23-NOV-2000.  
XX  
XX 15-MAY-2000; 2000WO-US013379.  
XX  
XX 14-MAY-1999; 99US-0134373P.  
XX  
XX (HUTC-) HUTCHINSON CANCER RES CENT FRED.  
XX  
XX Roberts J, Kelly B;  
XX  
XX WPI; 2001-024998/03.  
XX N-PSDB; AAC85204.  
XX  
XX Functionally inactivating expression of plant D-like cyclin inhibitor  
XX gene for producing a hyperplastic variant plant, modulating the growth  
XX and/or yield of plants, and increasing the proportion of dividing cells.  
XX  
XX Example 1; Page 40-41; 50pp; English.  
XX

CC The sequence given in AAB47004 represents a plant D1 cyclin inhibitor,  
CC BRO3. The DNA encoding this sequence was isolated using a yeast two  
CC hybrid screen. The BRO3 protein was found to contain a seven amino acid  
CC sequence cyclin binding domain similar to that of BRO1, BRO2 and BRO4  
CC (see also AAB47005-6). The DNA encoding this sequence is homologous to a  
CC sequence present in a D-like cyclin inhibitor gene and when integrated at  
CC the corresponding locus, functionally inactivates plant D-like cyclin  
CC inhibitor protein expression. The BRO4 coding sequence may be used to  
CC produce a hyperplastic variant plant, increase the growth rate of a  
CC plant, or increase the proportion of dividing cells in a plant cell  
CC population, relative to a wild-type plant, by functionally inactivating  
CC the expression of a plant D-like cyclin inhibitor gene in a plant. BRO4  
CC is useful for increasing the proportion of dividing cells in a plant cell  
CC population comprising protoplasts, seeds, root cells, meristem cells or  
CC leaf cells  
XX  
SQ Sequence 206 AA;  
Query Match 17.6%; Score 184; DB 4; Length 206;  
Best Local Similarity 30.4%; Pred. No. 1.4e-07;  
Matches 69; Conservative 43; Mismatches 73; Indels 42; Gaps 14;  
QY 1 PRDLPKNPREKMSERKRELAEEASTSFSPKTKTLNDSSSDSPDSDHVDVFAVSSSS- 59  
DB 1 PRDLP-----RDVVEGVTT-TTKRRKMEEVLD-LVESRIILSPCVQATNR 46  
QY 60 ---VASSAALASDECSVTIGGEES-----DOSSSISGCFTSSEKIAKNSSSFG 106  
DB 47 GGVARNASAGASETSVIVRRRDSPPVEQCQIEEDSSVSC-CSTSEK--SKRIEF- 102  
QY 107 VLELDHQ-IETETSTFTSNTFRKETSPPVSEGLGETTTEMSSSATKQKQGVKTKPTA 165  
DB 103 VDLEENNGDDRETETS-WIYDNLK--SEESNMDSVVAVESVRRRLRSLHETVKE 159  
QY 166 AEIEDLSELESPPDDKKQFIE---KYNFDVNDPEL-BGRYKWDRL 208  
DB 160 AELEDFQVAKK-DLRNKLCSMKYNDFEKFDEPLGGRYEHWKL 204  
RESULT 9  
AAW98179  
ID AAW98179 standard; protein; 209 AA.  
XX  
AC AAW98179;  
XX  
XX 05-JUL-1999 (first entry)  
XX  
XX Arabidopsis cyclin-dependent kinase inhibitor FL39.  
XX  
XX Cyclin-dependent kinase inhibitor; CDK inhibitor; CKI; CDKI; FL39;  
XX plant development; transgenic plant; cell cycle; growth regulator;  
XX herbicide.  
XX  
XX Arabidopsis thaliana.  
XX  
XX Key Location/Qualifiers  
XX Region 4..14  
XX /note= "repeated motif"  
XX Peptide 23..26  
XX /note= "putative nuclear localisation signal"  
XX Region 68..78  
XX /note= "repeated motif"  
XX Protein 75..209  
XX /note= "this protein region is specifically claimed in  
XX Claim 1(c)"  
XX Region 79..98  
XX /note= "PEST-rich region, characteristic of unstable  
XX proteins"  
XX  
XX WO9914331-A2.  
XX  
XX 25-MAR-1999.  
XX





PR	02-JUL-1999;	99US-0142055P.	PR	22-SEP-1999;	99US-0155139P.
PR	06-JUL-1999;	99US-0142390P.	PR	23-SEP-1999;	99US-0155486P.
PR	08-JUL-1999;	99US-0142803P.	PR	24-SEP-1999;	99US-0155659P.
PR	09-JUL-1999;	99US-0142920P.	PR	28-SEP-1999;	99US-0156458P.
PR	12-JUL-1999;	99US-0142977P.	PR	29-SEP-1999;	99US-0156596P.
PR	13-JUL-1999;	99US-0143342P.	PR	04-OCT-1999;	99US-0157117P.
PR	14-JUL-1999;	99US-0143624P.	PR	05-OCT-1999;	99US-0157753P.
PR	15-JUL-1999;	99US-0144005P.	PR	06-OCT-1999;	99US-0157865P.
PR	16-JUL-1999;	99US-0144085P.	PR	07-OCT-1999;	99US-0158029P.
PR	16-JUL-1999;	99US-0144325P.	PR	08-OCT-1999;	99US-0158232P.
PR	19-JUL-1999;	99US-0144331P.	PR	12-OCT-1999;	99US-0158369P.
PR	19-JUL-1999;	99US-0144332P.	PR	13-OCT-1999;	99US-0159293P.
PR	19-JUL-1999;	99US-0144333P.	PR	13-OCT-1999;	99US-0159294P.
PR	19-JUL-1999;	99US-0144334P.	PR	14-OCT-1999;	99US-0159295P.
PR	19-JUL-1999;	99US-0144335P.	PR	14-OCT-1999;	99US-0159329P.
PR	20-JUL-1999;	99US-0144352P.	PR	14-OCT-1999;	99US-0159330P.
PR	20-JUL-1999;	99US-0144632P.	PR	14-OCT-1999;	99US-0159331P.
PR	20-JUL-1999;	99US-0144884P.	PR	14-OCT-1999;	99US-0159637P.
PR	21-JUL-1999;	99US-0144814P.	PR	14-OCT-1999;	99US-0159638P.
PR	21-JUL-1999;	99US-0145086P.	PR	18-OCT-1999;	99US-0159584P.
PR	21-JUL-1999;	99US-0145088P.	PR	21-OCT-1999;	99US-0160741P.
PR	21-JUL-1999;	99US-0145085P.	PR	21-OCT-1999;	99US-0160767P.
PR	22-JUL-1999;	99US-0145087P.	PR	21-OCT-1999;	99US-0160768P.
PR	22-JUL-1999;	99US-0145089P.	PR	21-OCT-1999;	99US-0160770P.
PR	22-JUL-1999;	99US-0145192P.	PR	21-OCT-1999;	99US-0160814P.
PR	23-JUL-1999;	99US-0145145P.	PR	21-OCT-1999;	99US-0160815P.
PR	23-JUL-1999;	99US-0145218P.	PR	22-OCT-1999;	99US-0160980P.
PR	23-JUL-1999;	99US-0145224P.	PR	22-OCT-1999;	99US-0160981P.
PR	26-JUL-1999;	99US-0145276P.	PR	22-OCT-1999;	99US-0160989P.
PR	27-JUL-1999;	99US-0145913P.	PR	25-OCT-1999;	99US-0161404P.
PR	27-JUL-1999;	99US-0145918P.	PR	25-OCT-1999;	99US-0161405P.
PR	28-JUL-1999;	99US-0145919P.	PR	25-OCT-1999;	99US-0161406P.
PR	28-JUL-1999;	99US-0145951P.	PR	26-OCT-1999;	99US-0161359P.
PR	02-AUG-1999;	99US-0146386P.	PR	26-OCT-1999;	99US-0161360P.
PR	02-AUG-1999;	99US-0146388P.	PR	26-OCT-1999;	99US-0161361P.
PR	03-AUG-1999;	99US-0146389P.	PR	28-OCT-1999;	99US-0161920P.
PR	03-AUG-1999;	99US-0147038P.	PR	28-OCT-1999;	99US-0161922P.
PR	04-AUG-1999;	99US-0147204P.	PR	28-OCT-1999;	99US-0161993P.
PR	04-AUG-1999;	99US-0147302P.	PR	29-OCT-1999;	99US-0162142P.
PR	05-AUG-1999;	99US-0147192P.			
PR	06-AUG-1999;	99US-0147260P.			
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Best Local Similarity 30.7%; Pred. No. 5.7e-07;

Matches 65; Conservative 44; Mismatches 73; Indels 30; Gaps 13;

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QY	72	SVTIGGEES-----DQSSSISSGCGFTSESKEIAKNSSSGVDLEDHQ-IETETET	120	
Db	65	VVIVRRDSPVVEEQCIEEDSSVSC-CSTSEEK--SKRIEF-VLLEENNGDDRETET	120	
QY	121	STFITSNFRKETSVPSEGLGETTTEMESSATRKQPGVKRKTPTAAEIEDLFSELESPOD	180	
Db	121	S-WIYDDLNK--SEESMNDSSVAVEDVESRRRLKSLHETVKEAELEDFFQVAEK--D	175	
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ID	AAG38486	standard; protein; 209 AA.		
XX				
AC	AAG38486;			
XX				
DT	18-OCT-2000	(first entry)		
XX				
DE	Arabidopsis thaliana	protein fragment SEQ ID NO: 47487.		
XX				
KW	Protein identification; signal transduction pathway; metabolic pathway;			
KW	hybridisation assay; genetic mapping; gene expression control; promoter;			

KW termination sequence.  
XX Arabidopsis thaliana.  
XX EP1033405-A2.  
XX PD 06-SEP-2000.  
XX 25-FEB-2000; 2000EP-00301439.  
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XX DE Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 98.
XX plant; transgenic; E2Fa/Dpa transcription factor; growth regulator;
KW animal feed product; thale cress; cell wall biosynthesis;
KW nitrogen metabolism; carbon metabolism.
XX Arabidopsis thaliana.
OS WO2004035798-A2.
XX PN
XX 29-APR-2004.
XX PD
XX 20-OCT-2003; 2003WO-EP011658.
XX PF
XX 18-OCT-2002; 2002EP-00079408.
XX PR
XX (CROP-) CROPDISEIGN NV.
XX PA
XX Inze D, De Veylder L, Vlieghe K;
XX PI
XX WPI: 2004-348466/32.
XX DR
XX N-PSDB; ADN72202.
XX
XX Altering plant characteristics, useful for producing plants for enzyme or
PT pharmaceutical production comprises modifying in a plant, expression of
PT one or more nucleic acids and/or modifying level or activity of one or
PT more proteins.
XX
XX Claim 1; SEQ ID NO 98; 134pp; English.
XX
XX This invention relates to a novel method for altering one or more plant
CC characteristics. Specifically, it refers to identifying genes that are up
CC - or down-regulated in transgenic plants overexpressing the heterodimeric
CC E2Fa/Dpa transcription factor of Arabidopsis and using these sequences to
CC alter plant characteristics accordingly. The present invention describes
CC generating transgenic plants for the production of growth regulators,
CC enzymes, therapeutics, pharmaceuticals and animal feed products, where
CC the altered plant characteristics are selected from increased yield or
CC biomass, enhanced survival capacity, stress tolerance, plant architecture
CC or physiology, altered endoreplication, biochemistry, signal
CC transduction, storage lipid mobilisation and/or altered photosynthesis,
CC each relative to the corresponding wild type plants. Accordingly, these
CC sequences can also be useful as positive or negative selectable markers
CC during transformation of cells or tissues. The identified genes play a
CC role in a variety of biological processes such as DNA replication, cell
CC wall biosynthesis, nitrogen and/ or carbon metabolism or they function as
CC transcription factors. This polypeptide sequence is thale cress protein
CC expressed by a gene upregulated 1.3 fold or more in plants overexpressing
CC the E2Fa/Dpa transcription factor, given in an exemplification of the
CC invention.
XX
XX Sequence 209 AA;
SQ
Query Match 16.9%; Score 177; DB 8; Length 209;
Best Local Similarity 30.7%; Pred. No. 5.7e-07;
Matches 65; Conservative 44; Mismatches 73; Indels 30; Gaps 13;
QY 16 KRRLAEASSTFSPLKTKLNDSDSPSHDIVFAVSSSS---VASSAALASDEC 71
DB 7 RERDVVEENGVT-TTVKRRKMEEBV-LVESRIILSPCVQATNRGGIVARNAGASETS 64
QY 72 SVTIGGEES-----DQSSSTSSGCFSTSESKEIAKNSSFGVDLEDHQ-ITEFET 120
DB 65 VVIVRRRDSPPVEEQCIIEEDSSVSC-CSTSEEK--SKRRTEF-VDLSENNGGDDRETET 120
QY 121 STFITSNFRKETSPPVSEGLGETTTBMESSATKRPQGVKTKPTAAETEDLFSESESPDD 180
DB 121 S-WIYDDLNK--SESSMNMDSSVAVEDVESRRRLKSLHEITVKEALEDFQVAEK--D 175
QY 181 KKKQFIE---KYNFIVNDEPL-EGRYKWDRL 208
DB 176 LRNKLLECMKYNFDFEKDEPLGGGRYEWVKL 207
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## RESULT 14

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AAAY44335
ID AAY44335 standard; protein; 191 AA.
XX
XX AC AAY44335;
XX
XX DT 29-FEB-2000 (first entry)
XX
XX DE Arabidopsis thaliana CDK inhibitor, ICK1.
XX
XX Cyclin-Dependent kinase inhibitor; CDK; Interactor of Cdc2 kinase 1;
KW ICK1; Cdc2a; D-class cyclin; CycD1; CycD2; CycD3; morphogenesis;
KW antisense construct; tissue-specific promoter; transgenic plant;
KW male sterility.
XX
XX OS Arabidopsis thaliana.
XX
XX FH Key Location/Qualifiers
XX Region 109..153
XX FT /note= "Important for interaction with CycD3"
XX
XX PN WO9964599-A1.
XX
XX PD 16-DEC-1999.
XX
XX PF 08-JUN-1999; 99WO-CA000532.
XX
XX PR 08-JUN-1998; 98CA-02235978.
XX
XX PR 31-DEC-1998; 98CA-02256121.
XX
XX (MIAC ) AGRIC & AGRIFOOD CANADA.
XX (UYSA ) UNIV SASKATCHEWAN TECHNOLOGIES INC.
XX (CANA ) NAT RES COUNCIL CANADA.
XX
XX Wang H, Powke LC, Crosby WL;
XX WPI: 2000-097540/08.
XX N-PSDB; AAZ29415.
XX
XX Modifying plant cell development using nucleic acid encoding inhibitor of
PT cyclin-dependent kinase, or corresponding antisense sequence, e.g. for
PT inducing male sterility.
XX
XX Claim 7; Fig 1; 58pp; English.
XX
XX The present sequence is A. thaliana Cyclin-Dependent kinase (CDK)
CC inhibitor, ICK1. Interactor of Cdc2 kinase 1 (ICK1) interacts with Cdc2a,
CC D-class cyclins, CycD1, CycD2 and CycD3. Growth, morphogenesis,
CC multiplication, enlargement, differentiation and maturation of plant
CC cells can be modified by transforming them with nucleic acid encoding CDK
CC inhibitor or antisense construct complementary to the CDK inhibitor gene,
CC operably linked to a tissue-specific promoter. The transgenic plants
CC exhibit alteration of traits such as petals, male sterility and ability
CC to set seeds
XX
XX Sequence 191 AA;
SQ
Query Match 16.8%; Score 175.5; DB 3; Length 191;
Best Local Similarity 26.7%; Pred. No. 6.8e-07;
Matches 59; Conservative 34; Mismatches 63; Indels 65; Gaps 9;
QY 16 KRRLAEASSTFSPLKTKLNDSDSPSHDIVFAVSSSSVASSAALASDEC SVTI 75
DB 7 KAKGIVEAGVSGSTYMLRSRR-----IVVRSEKS-----SSVSV 41
QY 76 GGBESDQSSSTSSGCFSTSESKEIAKNSSFGVDLEDHQIETETETSTF-----ITSNF 128
DB 42 VGD-----NGVSSSC--SGSNEYKKEL---IHLEEDKDGDTETSTYRGTGKRLFENL 91
QY 129 RKE-----TSPVSEGL-----GETTMESSATKRPQGVKTKPTAAE 167
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Db 92 REBEKEELSKSMENYSSEFESAVKESLDCSCGRKTMEETVTAEEBEKAKLMTMPTESE 151  
QY 168 IEDLFSELESPPDKKQFKTEKYNFDIVNDEPLEGRYKWDRL 208  
Db 152 IEDFFVEAEK--QLKEKFKKKYNFDPEKEKPLEGRYEWVKL 190

RESULT 15  
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ID AAG15426 standard; protein; 191 AA.  
XX AC AAG15426;  
XX DT 17-OCT-2000 (first entry)  
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 15674.  
XX KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX OS Arabidopsis thaliana.  
XX EP1033405-A2.  
XX PD 06-SEP-2000.  
XX PF 25-FEB-2000; 2000EP-00301439.  
XX 25-FEB-1999; 99US-0121825P.  
PR 05-MAR-1999; 99US-0123180P.  
PR 09-MAR-1999; 99US-0123548P.  
PR 23-MAR-1999; 99US-0125788P.  
PR 25-MAR-1999; 99US-0126264P.  
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PR 13-AUG-1999; 99US-0148565P.  
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PR 17-AUG-1999; 99US-0149175P.  
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PR 20-AUG-1999; 99US-0149722P.  
PR 20-AUG-1999; 99US-0149723P.  
PR 20-AUG-1999; 99US-0149929P.  
PR 23-AUG-1999; 99US-0149902P.  
PR 23-AUG-1999; 99US-0149930P.  
PR 25-AUG-1999; 99US-0150566P.  
PR 26-AUG-1999; 99US-0150884P.  
PR 27-AUG-1999; 99US-0151065P.  
PR 27-AUG-1999; 99US-0151066P.  
PR 27-AUG-1999; 99US-0151080P.  
PR 30-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154779P.  
PR 22-SEP-1999; 99US-0155139P.  
PR 23-SEP-1999; 99US-0155486P.  
PR 24-SEP-1999; 99US-0155659P.  
PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.  
PR 05-OCT-1999; 99US-0157533P.  
PR 06-OCT-1999; 99US-0157865P.  
PR 07-OCT-1999; 99US-0158029P.  
PR 08-OCT-1999; 99US-0158232P.  
PR 12-OCT-1999; 99US-0158369P.  
PR 13-OCT-1999; 99US-0159293P.  
PR 13-OCT-1999; 99US-0159294P.  
PR 13-OCT-1999; 99US-0159295P.  
PR 14-OCT-1999; 99US-0159329P.  
PR 14-OCT-1999; 99US-0159330P.  
PR 14-OCT-1999; 99US-0159331P.  
PR 14-OCT-1999; 99US-0159637P.  
PR 14-OCT-1999; 99US-0159638P.  
PR 18-OCT-1999; 99US-0159584P.  
PR 21-OCT-1999; 99US-0160741P.  
PR 21-OCT-1999; 99US-0160767P.  
PR 21-OCT-1999; 99US-0160768P.  
PR 21-OCT-1999; 99US-0160770P.  
PR 21-OCT-1999; 99US-0160814P.  
PR 21-OCT-1999; 99US-0160815P.  
PR 22-OCT-1999; 99US-0160980P.  
PR 22-OCT-1999; 99US-0160981P.  
PR 22-OCT-1999; 99US-0160989P.  
PR 25-OCT-1999; 99US-0161404P.  
PR 25-OCT-1999; 99US-0161405P.  
PR 25-OCT-1999; 99US-0161406P.  
PR 26-OCT-1999; 99US-0161359P.  
PR 26-OCT-1999; 99US-0161360P.  
PR 26-OCT-1999; 99US-0161361P.  
PR 26-OCT-1999; 99US-0161361P.  
PR 28-OCT-1999; 99US-0161920P.  
PR 28-OCT-1999; 99US-0161992P.  
PR 28-OCT-1999; 99US-0161993P.  
PR 29-OCT-1999; 99US-0162142P.

Query Match 16.8%; Score 175.5; DB 3; Length 191;  
Best Local Similarity 26.7%; Pred. No. 6.8e-07;  
Matches 59; Conservative 34; Mismatches 63; Indels 65; Gaps 9;  
QY 16 RKRELAEEASSTSFPLKTKLNDSSDPDSDHVIFAVSSSVASSAALASDECSTYI 75  
DB 7 KAKGIVEAGVSTYMQLRSR-----IVYVRSEK-----SSVSV 41  
QY 76 GGEESDQSSISGCGFTSEKIAKNSSFGVDLEDHQIETETSTP-----ITSNF 128

Db 42 VGD-----NGVSSSC--SGSNEYKKEL---IHLEEDKOGDTETSYVRRGTTKKLFFNL 91  
QY 129 RKE-----TSPVSEGL-----GTTTMESSSATKKKQPGVRKTPAAE 167  
Db 92 REEKEELSKSMENYSSEFSAVKESLDCCSGRKTWEETVTAEEEEKAKLWEMPTIESE 151  
QY 168 IEDLSELESFDDKKKQFIEKYNFDIYNDBPLEGRYKWDRL 208  
Db 152 IEDFFVEAEK--QLKEKFKKKYNFDFEKEKPLEGRYEWVKL 190

Search completed: September 30, 2005, 11:34:01  
Job time : 83 secs

Result No.	Score	Query Match	Length	DB	ID	Description	
1	177	16.9	209	4	US-09-526-597D-2	Sequence 2, Appli	
2	152	14.5	222	4	US-09-526-597D-4	Sequence 4, Appli	
3	136.5	13.1	223	4	US-09-526-597D-6	Sequence 6, Appli	
4	133.5	12.8	327	4	US-09-526-597D-34	Sequence 34, Appli	
5	132.5	12.7	414	1	US-07-667-276A-4	Sequence 4, Appli	
6	128	12.2	2137	3	US-09-134-001C-4463	Sequence 4463, Ap	
7	121.5	11.6	286	4	US-09-248-796A-22818	Sequence 22818, A	
8	116.5	11.1	312	4	US-09-270-767-33271	Sequence 33271, A	
9	116.5	11.1	312	4	US-09-270-767-48488	Sequence 48488, A	
10	116	11.1	402	4	US-09-248-796A-18910	Sequence 18910, A	
11	114.5	11.0	414	4	US-09-248-796A-19046	Sequence 19046, A	
12	113	10.8	669	4	US-09-107-532A-6532	Sequence 6532, Ap	
13	112.5	10.8	491	4	US-09-107-532A-6115	Sequence 6115, Ap	
14	111	10.6	699	4	US-09-248-796A-23200	Sequence 23200, A	
15	110.5	10.6	685	4	US-09-248-796A-20197	Sequence 20197, A	
16	109.5	10.5	1306	4	US-09-538-092-330	Sequence 330, App	
17	107.5	10.3	165	4	US-09-248-796A-23180	Sequence 23180, A	
18	107.5	10.3	382	4	US-09-248-796A-17276	Sequence 17276, A	
19	107	10.2	273	4	US-09-248-796A-25975	Sequence 25975, A	
20	106.5	10.2	461	4	US-09-248-796A-23039	Sequence 23039, A	
21	106	10.1	145	3	US-08-808-599A-41	Sequence 41, Appl	
22	106	10.1	556	4	US-09-248-796A-22338	Sequence 22338, A	
23	105	10.0	687	4	US-09-248-796A-23026	Sequence 23026, A	
24	105	10.0	722	4	US-09-592-714-22	Sequence 22, Appl	
25	104	10.0	161	3	US-09-134-001C-4577	Sequence 4577, Ap	
26	104	10.0	385	4	US-09-248-796A-21836	Sequence 21836, A	
27	104	10.0	539	4	US-09-248-796A-16542	Sequence 16542, A	

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; FILE REFERENCE: 1187-2
; CURRENT APPLICATION NUMBER: US/09/526,597D
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-526-597D-4

Query Match      14.5%; Score 152; DB 4; Length 222;
Best Local Similarity 30.6%; Pred. No. 9.1e-06;
Matches 59; Conservative 24; Mismatches 70; Indels 40; Gaps 11;

QY 16 RKRLAEASSTSFPLKTKLNDSSDPSHDVIVFAVSSSVASSAALADECSVTI 75
Db 62 KSRRL--EKPSLIEPKQPPRVHRSGIKESGRS--RVDVSNVVPVAQSS--NEDEC--- 112
QY 76 GGEESDQSSISGCGFTSESKEIAKNSSSFGVDLEDHQIETETETSTITSNFRKETSPV 135
Db 113 ----FDNFVSVQVSC-----GENSLGF-----ESRHSSTRESTPCNFV-----EDMEI 150
QY 136 SEGGETTEMESSATK---RKQGVKRTPTAAEIEDLFSELESPPDDKKQKQFIKYNFD 192
Db 151 MVTGSSSTRSM--CHATKEYTREQDNV--IPTTSEMEEFFAYAE--QQQORLFWEKYNFD 204
QY 193 IVNDEPLEGRYK 205
Db 205 IVNDIPLSGRYEW 217

RESULT 3
US-09-526-597D-6
; Sequence 6, Application US/09526597D
; Patent No. 6710227
; GENERAL INFORMATION:
; APPLICANT: De Veylder, Lieven
; APPLICANT: De Almeida, Janice
; APPLICANT: Landrieu, Isabelle
; TITLE OF INVENTION: Cyclin-dependent kinase inhibitors and uses thereof
; FILE REFERENCE: 1187-2
; CURRENT APPLICATION NUMBER: US/09/526,597D
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-526-597D-6

Query Match      13.1%; Score 136.5; DB 4; Length 223;
Best Local Similarity 23.5%; Pred. No. 0.00022;
Matches 54; Conservative 45; Mismatches 82; Indels 49; Gaps 10;

QY 11 KMSERKREAEAGSTSFSLKTKLNDSSDPSHDVI-----VFAVSSS----- 58
Db 9 KSKSESPNSPTPSPSPPTIT--TNSPPPTPNSSDGVKTRTARTLALENNQNQL 67
QY 59 SVASSA-----ALADECSVTIGGEESDQSSISGCGFTSESKEIAKNSSSFGV 107
Db 68 SVSSDYLQLRNRLKRLIRQHSKRNKNGDGNPKSPI--GDSIAEKTQKSPENPA 125
QY 108 DLEDHQIETETSTFTITSNFRKETSPV-----SEGLGE-----TTTEMSSSATKQKPG 158
Db 126 EFKENAEDTERSA-----RETPVHLINRADVLPRPPRITRTPTFEANPKTEQPT 176
QY 159 VRKTPAAEIEDLFSELESPPDDKKQKQFIKYNFDIVNDEPLEGRYKWDRL 208
Db 177 I---PISREFEFCAKHEA--EQQREFWEKYNFDVPTQPLGRYEWK 221

; FILE REFERENCE: 1187-2
; CURRENT APPLICATION NUMBER: US/09/526,597D
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-526-597D-34

Query Match      12.8%; Score 133.5; DB 4; Length 327;
Best Local Similarity 20.2%; Pred. No. 0.00067;
Matches 57; Conservative 45; Mismatches 79; Indels 101; Gaps 11;

QY 1 PRDLP-----KNPREKMKSEKRELAEEASS-----TSFSPKTKTKL 37
Db 71 PSSLPPTSASPNPPSKQKMKKQKQMDGCVLQLRSRRLQKPPVIVIRSTKRRKQRR 130
QY 38 NDSSDSSPDSDHDVIVFAVSSSVASSAALADECSVTIGGEESDQSSISGCGFTSESKE 97
Db 131 NETCGRPNPRS-----NLDISIRGDSRSDSVSVFVGKDKDLISEIN----- 174
QY 98 IAKNSSSFG---VDLEDHQIET---ETETSTFTITSNFRKE--TSPVSESG---LGTTTT 144
Db 175 ---KDPTFGQNFDFLEEHQTOSFRTRESTPCSLIRPEIMTTPGSGSTKLNICVSESNQ 231
QY 145 EMESSATKQKQGVKRTPTAAEIEDLFSELESPPDDKKKQKQFIK----- 188
Db 232 REDSLRSRSHRR-----PTTPMEDPEFPGAE--EEQKQFIKQVFFRFGVCSVLLVMSF 283
QY 189 -----YNFDIVNDEPLEGRYKWDRL 208
Db 284 QFVLFFSFGVSLVMSVNSPFRYFNPDPVNEQPLPGRFWEWKV 325

RESULT 5
US-07-667-276A-4
; Sequence 4, Application US/07667276A
; Patent No. 5470971
; GENERAL INFORMATION:
; APPLICANT: Kondo, Keiji
; APPLICANT: Inouye, Masaayori
; TITLE OF INVENTION: STRESS-INDUCED PROTEINS, GENES CODING
; TITLE OF INVENTION: THEREFOR, TRANSFORMED CELLS OF ORGANISMS, METHODS AND
; TITLE OF INVENTION: APPLICATIONS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weiser & Associates
; STREET: 230 S. Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/667,276A
; FILING DATE: 11-MAR-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
```



; NAME: Weiser, Gerard J.  
; REGISTRATION NUMBER: 19,763  
; REFERENCE/DOCKET NUMBER: 377,5351P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-875-8383  
; TELEFAX: 215-875-8394  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 414 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-667-276A-4

Query Match 12.7%; Score 132.5; DB 1; Length 414;  
Best Local Similarity 29.3%; Pred. No. 0.0011;  
Matches 61; Conservative 25; Mismatches 73; Indels 49; Gaps 9;

QY 7 NPREKMSRKRRLAEASSTSFPLKTKLNDSSDPDHDVIVFAVSSSVASSAAL 66  
Db 10 NKKEVKASKQAKK--EKAKAVSS-----SSSSSSSS-----SSSESESE 50

QY 67 ASDCVTTIGGERSDQSSISGCFSTSES-----KEIAKNSSSGFVD-LEDHQIETET 120  
Db 51 SESESSSSSSSDSSSSSSSSSSSSSS--DSEAEFTKKEEKDSSSSSDSSDSEDEEEKEE 107

QY 121 STFITNSFRKETSVPSEGLGETTEMESSSATKRKQGVKKTPTAAAEIEDLFSELESPD 180  
Db 108 TKKEESKSSSSSSSSSSSDSSSEKESNDKKRS-----EDABEEDEESS 155

QY 181 KKKQFIKYNFDIVNDP---LEGRYKW 205  
Db 156 NKKQKNEE-----TEEPATIFVGRLSW 177

RESULT 6  
US-09-134-001C-4463  
; Sequence 4463, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; PRIOR FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 4463  
; LENGTH: 2137  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-4463

Query Match 12.2%; Score 128; DB 3; Length 2137;  
Best Local Similarity 25.6%; Pred. No. 0.027;  
Matches 45; Conservative 35; Mismatches 66; Indels 30; Gaps 6;

QY 24 ASSTSFPLKTKLNDSS-----SDSSPDHDVIVFAVSSSVASSAALASDE 70  
Db 1868 SASTSLSGSTSTSVSDSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSD 1927

QY 71 CSVTIGGERSDQSSISGCFSTSESKEIAKNSSFGVDLEDHQIETETSTFTNSFRK 130  
Db 1928 SASTSTSEASTSTSVSES--DSESTSVSESSST-----SVSDSTSTSTSTSTSTSD 1974

QY 131 ETPSPVSEGLGETTEMESSSATKRKQGVKKTPTAAAEIEDLFSELESPDCKKQFI 186  
Db 1975 TSTSESESTSESTSVSESSSTSTSDS---SSTSTSTMTSETFTIS-QSPINSESQFI 2026

## RESULT 7

US-09-248-796A-22818  
; Sequence 22818, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA  
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 22818  
; LENGTH: 286  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-09-248-796A-22818

Query Match 11.6%; Score 121.5; DB 4; Length 286;  
Best Local Similarity 28.3%; Pred. No. 0.0065;  
Matches 39; Conservative 27; Mismatches 61; Indels 11; Gaps 3;

QY 12 KMSERKRLAEASSTSFPLKTKLNDSSDPDHDVIVFAV---SSSSVASSAALAS 68  
Db 152 QQQSQSQSQSQSTSTSQAPLSTMSDNTSFVSPDSTLLVSAATTTSSSSSSSLTP 211

QY 69 DECSVTIGGEESDQ-----SSISGCFSTSESKEIAKNSSFGVDLEDHQIETETSTFTI 124  
Db 212 STSDVTTSSASSSPSTTTSSSTAFSSSTTETSSATSSSTSSSTSSSILSTQNTSLSS 271

QY 125 TSNFRKETSPVSEGLGET 142  
Db 272 NTSF-----SVSHGAGET 285

## RESULT 8

US-09-270-767-33271  
; Sequence 33271, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 33271  
; LENGTH: 312  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-33271

Query Match 11.1%; Score 116.5; DB 4; Length 312;  
Best Local Similarity 22.9%; Pred. No. 0.02;  
Matches 49; Conservative 32; Mismatches 94; Indels 39; Gaps 6;

QY 20 LAEASSTSFPLKTKLNDSSDPD-----SHDVIVFAVSSSVVA 61  
Db 6 LSSDSTDTAATAASDNTDITDGTDESTDGSNNASTEGSTEGASEDTTISTESSGSTE 65

QY 62 SAAALASDECSVTIGGERSDQSSISGCF-----TSESKEIA-KNSSSFGVDLEDHQ 113  
Db 66 STDALASDG-STTEGSTVEDLSSSTSSDVTSSTITDSSPSTEVSGSTSSSSTDGSSTD 124

QY 114 IETETSTFTTNSFRKETSPVSEGLGET-----TTEMESSSATKRKQGVKKTPT 164  
Db 125 ASSTASSTDVTES---TDSTVSGGSTPTTESGPTTEESTTEGSTDSTDL 181





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; LENGTH: 699
; TYPE: PRT
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (487),(699)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknown
US-09-248-796A-23200

Query Match      10.6%; Score 111; DB 4; Length 699;
Best Local Similarity 21.6%; Pred. No. 0.19;
Matches 46; Conservative 38; Mismatches 61; Indels 68; Gaps 7;

QY      3  DLPKNPKEKNGSERKRELAEEASSTSTSPPLKTKLNDSSDSDSHDVIVFAVSS 57
Db      411  DKQSP-----KRVSDQASSNQEIVDNPTATKISESSSEEE-----I 451

QY      58  SSVASSAALADECVTTGGESDQSSISGCGFTSESKEIAKNSSSFGVDL---EDHQI 114
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
452  ANNPTPTMDIDESSSSGEEEMASNTSKVDSGASXNDKEVANNPTKVSDGLASSNDEEI 511

QY      115  ETETSTFI----TSNFKETSPVSEGLGETTTEMESSAT-----KKQP----- 157
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
512  SNNPETLTKVSDSSSSDEEASDVAVMDGTSGSDTESSTNPETPPKLNQKQPIANAG 571

QY      158  -----GVRKTPATAA 166
Db      : : : : :

572  GDKVSNKSEIMVAPLPIATPRVQGLALTPTAS 604

RESULT 15
US-09-248-796A-20197
; Sequence 20197, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 20197
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-20197

Query Match      10.6%; Score 110.5; DB 4; Length 685;
Best Local Similarity 25.6%; Pred. No. 0.2;
Matches 44; Conservative 32; Mismatches 73; Indels 23; Gaps 5;

QY      14  SERKREL-----AERASSTSPSLAKTKLNDSSDSDSHDVIVFAVSSS-----VASSA 64
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
71  SEQRSSIPIMSSDESSRESIGTILSEESSDSIPTFTRYWSPGMSRHYTNSTE 130

QY      65  ALASDECSTVTTGGEESDQSS-----SISGCGFTSESKEIAKNSSSFGVDLEDHQIETET 120
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
131  TLVSDVLSSVAGDITSESSVSIVSESVTSSES--VASESVTAVSDISDIYTTSEVVS 188

QY      121  -----STFTSNFRKETSPVSEGLGETTTEMESSSATKRPQGVKTPPT 164
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
189  TSDSKIVFPSTVPSPSEQRSSIPIMSSDESSRESRESSTGILSEENSDSIPT 240

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Search completed: September 30, 2005, 11:36:35  
Job time : 28 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 30, 2005, 11:32:43 ; Search time 411 Seconds  
(without alignments)  
211.093 Million cell updates/sec

Title: US-09-980-758A-8  
Perfect score: 1045  
Sequence: 1 PRDLPNPREKKMSERKREL.....NFDIYNDEPLEGRYKWDRLX 209

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1846076 seqs, 415116000 residues

Total number of hits satisfying chosen parameters: 1846076

Minimum DB seq length: 0  
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Maximum Match 100%  
Listing first 45 summaries

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12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/2/pubpaa/US10E\_PUBCOMB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/2/pubpaa/US11A\_PUBCOMB.pep.\*  
20: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	1007	96.4	212 9 US-09-733-507-12	Sequence 12, Appl
2	1007	96.4	212 15 US-10-451-139-11	Sequence 11, Appl
3	969	92.7	196 15 US-10-451-139-22	Sequence 22, Appl
4	351.5	33.6	207 15 US-10-451-139-12	Sequence 12, Appl
5	346.5	33.2	195 15 US-10-451-139-23	Sequence 23, Appl
6	341	32.6	208 9 US-09-733-507-13	Sequence 13, Appl
7	210.5	20.1	176 15 US-10-424-599-212181	Sequence 212181,
8	177	16.9	46 17 US-10-890-629-59	Sequence 59, Appl
9	177	16.9	209 15 US-10-688-291-2	Sequence 2, Appl
10	177	16.9	209 15 US-10-451-139-19	Sequence 19, Appl
11	176.5	16.9	191 9 US-09-733-507-10	Sequence 10, Appl

12	175.5	16.8	191	9 US-09-733-507-2	Sequence 2, Appl
13	175.5	16.8	191	15 US-10-451-139-2	Sequence 2, Appl
14	172	16.5	205	15 US-10-424-599-182928	Sequence 182928,
15	171.5	16.4	224	15 US-10-424-599-210190	Sequence 210190,
16	168.5	16.1	196	9 US-09-733-507-16	Sequence 16, Appl
17	168.5	16.1	196	15 US-10-451-139-15	Sequence 15, Appl
18	162.5	15.6	289	15 US-10-451-139-17	Sequence 17, Appl
19	159	15.2	176	9 US-09-733-507-11	Sequence 11, Appl
20	159	15.2	176	15 US-10-451-139-10	Sequence 10, Appl
21	155	14.8	222	15 US-10-451-139-21	Sequence 21, Appl
22	153.5	14.7	217	16 US-10-425-115-254155	Sequence 254155,
23	153.5	14.7	217	17 US-10-890-629-4	Sequence 4, Appl
24	153.5	14.7	255	15 US-10-425-114-61054	Sequence 61054, A
25	153	14.6	262	15 US-10-333-006-10	Sequence 10, Appl
26	153	14.6	417	16 US-10-437-963-195115	Sequence 195115,
27	152	14.5	222	15 US-10-688-291-4	Sequence 4, Appl
28	150.5	14.4	137	15 US-10-451-139-13	Sequence 13, Appl
29	149	14.3	194	15 US-10-333-006-44	Sequence 44, Appl
30	149	14.3	194	16 US-10-437-963-120870	Sequence 120870,
31	148	14.2	213	17 US-10-890-629-2	Sequence 2, Appl
32	148	14.2	248	15 US-10-425-114-59718	Sequence 59718, A
33	147.5	14.1	137	9 US-09-733-507-14	Sequence 14, Appl
34	144.5	13.8	212	16 US-10-425-115-268129	Sequence 268129,
35	141.5	13.5	205	15 US-10-424-599-235800	Sequence 235800,
36	138.5	13.3	225	16 US-10-437-963-198574	Sequence 198574,
37	138.5	13.3	406	16 US-10-451-467A-262	Sequence 262, App
38	136.5	13.1	223	15 US-10-688-291-6	Sequence 6, Appl
39	135.5	13.0	95	16 US-10-767-701-36263	Sequence 36263, A
40	134	12.8	218	16 US-10-437-963-128205	Sequence 128205,
41	134	12.8	254	17 US-10-890-629-12	Sequence 12, Appl
42	134	12.8	256	9 US-09-993-308-2	Sequence 2, Appl
43	134	12.8	256	11 US-09-993-808B-2	Sequence 2, Appl
44	133.5	12.8	252	16 US-10-425-115-223026	Sequence 223026,
45	133.5	12.8	327	15 US-10-688-291-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1

US-09-733-507-12  
; Sequence 12, Application US/09733507  
; Patent No. US20010025379A1  
; GENERAL INFORMATION:  
; APPLICANT: Agriculture and Agri-Food Canada; The University of Saskatchewan  
; TITLE OF INVENTION: Cyclin Dependant Kinase Inhibitors as Plant Growth  
; TITLE OF INVENTION: Regulators  
; FILE REFERENCE: 81601-3  
; CURRENT APPLICATION NUMBER: US/09/733,507  
; CURRENT FILING DATE: 2000-12-02  
; PRIOR APPLICATION NUMBER: CA 2,256,121  
; PRIOR FILING DATE: 1998-12-31  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 212  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-09-733-507-12

Query Match	96.4%	Score 1007;	DB 9;	Length 212;
Best Local Similarity	99.5%	Pred. No. 1.7e-68;		
Matches 202;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	6	KNPREKKMSERKRELAEEASSTSFPLKTKLNDSSDSDSPDSDHIVFAVSSSSVASSAA	65	
DB	10	KNPREKKMSERKRELAEEASSTSFPLKTKLNDSSDSDSPDSDHIVFAVSSSSVASSAA	69	
QY	66	LASDSCSVTIGGEEDQSSISGGCFTSESKIAKNSSFGVDLEDHQIETETSTFTT	125	
DB	70	LASDSCSVTIGGEEDQSSISGGCFTSESKIAKNSSFGVDLEDHQIETETSTFTT	129	
QY	126	SNFRKETSPVSEGLGETTMESSATKRKOPGVKRTPTAAEIEDLFSELESPDDKKQF	185	

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Db 130 SNFRKETSPLVSGELGTTTMESSATKRKQPGVRKTPATAAEIEDLFSELESQDDKKQF 189
Qy 186 TEKYNFDIVNDEPLEGRYKWDRL 208
Db 190 TEKYNFDIVNDEPLEGRYKWDRL 212

RESULT 2
US-10-451-139-11
; Sequence 11, Application US/10451139
; Publication No. US20040098763A1
; GENERAL INFORMATION:
; APPLICANT: WANG, HONG
; APPLICANT: ZHOU, YONGMING
; APPLICANT: FOWKE, LARRY C.
; APPLICANT: HER MAJESTY IN RIGHT OF CANADA AS REPRESENTED BY THE MINISTER OF
; APPLICANT: AGRICULTURE AND AGRI-FOOD CANADA
; TITLE OF INVENTION: MODULATION OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR
; FILE REFERENCE: 4810-62237
; CURRENT APPLICATION NUMBER: US/10/451,139
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: WO PCT/CA01/01825
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,908
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-451-139-11

Query Match 96.4%; Score 1007; DB 15; Length 212;
Best Local Similarity 99.5%; Pred. No. 1.7e-68;
Matches 202; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 KNPREKKMSERKRELAERASSTSFPLKTKLNDSSDSPSHDVIVFAVSSSSVASSAA 65
Db 10 KNPREKKMSERKRELAERASSTSFPLKTKLNDSSDSPSHDVIVFAVSSSSVASSAA 69

Qy 66 LASDCSVTIGGEESDQSSISGGCFTSESKEIAKNSSSFGVDLEDHQIETETSTFIT 125
Db 70 LASDCSVTIGGEESDQSSISGGCFTSESKEIAKNSSSFGVDLEDHQIETETSTFIT 129

Qy 126 SNFRKETSPLVSGELGTTTMESSATKRKQPGVRKTPATAAEIEDLFSELESQDDKKQF 185
Db 130 SNFRKETSPLVSGELGTTTMESSATKRKQPGVRKTPATAAEIEDLFSELESQDDKKQF 189

Qy 186 TEKYNFDIVNDEPLEGRYKWDRL 208
Db 190 TEKYNFDIVNDEPLEGRYKWDRL 212

RESULT 3
US-10-451-139-22
; Sequence 22, Application US/10451139
; Publication No. US20040098763A1
; GENERAL INFORMATION:
; APPLICANT: WANG, HONG
; APPLICANT: ZHOU, YONGMING
; APPLICANT: FOWKE, LARRY C.
; APPLICANT: HER MAJESTY IN RIGHT OF CANADA AS REPRESENTED BY THE MINISTER OF
; APPLICANT: AGRICULTURE AND AGRI-FOOD CANADA
; TITLE OF INVENTION: MODULATION OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR
; FILE REFERENCE: 4810-62237
; CURRENT APPLICATION NUMBER: US/10/451,139
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: WO PCT/CA01/01825
; PRIOR FILING DATE: 2001-12-18
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; PRIOR APPLICATION NUMBER: US 60/255,908
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-451-139-22

Query Match 92.7%; Score 969; DB 15; Length 196;
Best Local Similarity 99.5%; Pred. No. 1.2e-65;
Matches 195; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 13 MSERKRELAERASSTSFPLKTKLNDSSDSPSHDVIVFAVSSSSVASSAALASDCS 72
Db 1 MSERKRELAERASSTSFPLKTKLNDSSDSPSHDVIVFAVSSSSVASSAALASDCS 60

Qy 73 VTIGGEESDQSSISGGCFTSESKEIAKNSSSFGVDLEDHQIETETSTFITSNFRKET 132
Db 61 VTIGGEESDQSSISGGCFTSESKEIAKNSSSFGVDLEDHQIETETSTFITSNFRKET 120

Qy 133 SPVSEGLGETTTEMESSATKRKQPGVRKTPATAAEIEDLFSELESQDDKKQFIEKYNFD 192
Db 121 SPVSEGLGETTTEMESSATKRKQPGVRKTPATAAEIEDLFSELESQDDKKQFIEKYNFD 180

Qy 193 IVNDEPLEGRYKWDRL 208
Db 181 IVNDEPLEGRYKWDRL 196

RESULT 4
US-10-451-139-12
; Sequence 12, Application US/10451139
; Publication No. US20040098763A1
; GENERAL INFORMATION:
; APPLICANT: WANG, HONG
; APPLICANT: ZHOU, YONGMING
; APPLICANT: FOWKE, LARRY C.
; APPLICANT: HER MAJESTY IN RIGHT OF CANADA AS REPRESENTED BY THE MINISTER OF
; APPLICANT: AGRICULTURE AND AGRI-FOOD CANADA
; TITLE OF INVENTION: MODULATION OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR
; FILE REFERENCE: 4810-62237
; CURRENT APPLICATION NUMBER: US/10/451,139
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: WO PCT/CA01/01825
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,908
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-451-139-12

Query Match 33.6%; Score 351.5; DB 15; Length 207;
Best Local Similarity 44.5%; Pred. No. 8.4e-19;
Matches 93; Conservative 30; Mismatches 57; Indels 29; Gaps 10;

Qy 9 REKKMSERKRELAERASSTSFPLKTKLNDSSD--GSPDSDHVDVIVFAVSSSSVASSAAL 66
Db 11 REMSETPKRUSEYEGSN-----IKRWRLDDDDVILRSPTR-----TLSSSSSSSLAYS 59

Qy 67 ASDE---CSVTIGGEESDQ--SSISGGCFTSESKEIAKNSSSFGVDLEDHQIETETST 122
Db 60 VSDSGGFCVSALSEEDDHLSSISGGCSSETNEIATRLPF--SDLEAHEI--SETEIST 116

Qy 123 FITSNFRKETSPLVSGELGET-----TTEMESSATKRKQPGVRKTPATAAEIEDLFSELE 176
Db 117 LLTNNFRKQIGISSENLGETAEMDSATTEMRDQRKTEKKK--MEKSPQOAEIDFFSAE 175
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QY 177 SPDDKKQFIEKYNFDIVNDEPLEGRYK 205  
Db 176 RYE--QKRFTKYNDIVNDTPLEGRYQW 202

## RESULT 5

US-10-451-139-23

; Sequence 23, Application US/104511139  
; Publication No. US20040098763A1

GENERAL INFORMATION:

APPLICANT: WANG, HONG

APPLICANT: ZHOU, YONGMING

APPLICANT: FOWKS, LARRY C.

APPLICANT: HER MAJESTY IN RIGHT OF CANADA AS REPRESENTED BY THE MINISTER OF

APPLICANT: AGRICULTURE AND AGRI-FOOD CANADA

TITLE OF INVENTION: MODULATION OF PLANT CYCLIN-DEPENDENT KINASE INHIBITOR

TITLE OF INVENTION: ACTIVITY

FILE REFERENCE: 4810-62237

CURRENT APPLICATION NUMBER: US/10/451,139

CURRENT FILING DATE: 2003-06-18

PRIOR APPLICATION NUMBER: WO PCT/CA01/01825

PRIOR FILING DATE: 2001-12-18

PRIOR APPLICATION NUMBER: US 60/255,908

PRIOR FILING DATE: 2000-12-18

NUMBER OF SEQ ID NOS: 23

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 23

LENGTH: 195

TYPE: PRT

ORGANISM: Arabidopsis thaliana

US-10-451-139-23

Query Match 33.2%; Score 346.5; DB 15; Length 195;  
Best Local Similarity 45.4%; Pred. No. 1.9e-18;  
Matches 93; Conservative 27; Mismatches 58; Indels 27; Gaps 10;

QY 13 MSERKRELAERASTSFSPPLKTKLNDSSD--SSPDSDHVIIVFAVSSSSVASSAALAE 70  
Db 1 MSETKPKRDSEYEG--SNIKMRLLDDDDVLRSPTR-----TLSSSSSSSLAYSVD 51

QY 71 ---CSVTIGGEESDQ--SSISGCGFTSESKEIAKNSSSGFVLEHDHQTETETSTFT 126  
Db 52 GGCFCVSLSEEDDHLSSISGCGSSSETNEIATRLPF--SDLEAHEI-SETEISTLLTN 108

QY 127 NFRKETSPPVSEGLGET-----TTMESSSATKRKQGVKRTPTAAEIEDLFSELESPPD 180  
Db 109 NFRKQGISSENIGETAEWDSATTMRDQKTEKKK-MEKSPTQAELEDDFFSAERYE- 166

QY 181 KKKQFIEKYNFDIVNDEPLEGRYK 205  
Db 167 -QKRFTKYNDIVNDTPLEGRYQW 190

## RESULT 6

US-09-733-507-13

Sequence 13, Application US/09733507

Patent No. US20010025379A1

GENERAL INFORMATION:

APPLICANT: Agriculture and Agri-Food Canada; The University of Saskatchewan

TITLE OF INVENTION: Cyclin Dependent Kinase Inhibitors as Plant Growth

TITLE OF INVENTION: Regulators

FILE REFERENCE: 81601-3

CURRENT APPLICATION NUMBER: US/09/733,507

CURRENT FILING DATE: 2000-12-02

PRIOR APPLICATION NUMBER: CA 2,256,121

PRIOR FILING DATE: 1998-12-31

NUMBER OF SEQ ID NOS: 16

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 13

LENGTH: 208

TYPE: PRT

ORGANISM: Arabidopsis thaliana

US-09-733-507-13

Query Match 32.6%; Score 341; DB 9; Length 208;

Best Local Similarity 44.3%; Pred. No. 5.3e-18;

Matches 93; Conservative 30; Mismatches 57; Indels 30; Gaps 11;

QY 9 REKKMSERKRELAERASTSFSPPLKTKLNDSSD--SSPDSDHVIIVFAVSSSSVASSAAL 66  
Db 11 REMSETKPKRDSEYEGSN-----IKMRLLDDDDVLRSPTR-----TLSSSSSSSLAYS 59

QY 67 ASDE---CSVTIGGEESDQ--SSISGCGFTSESKEIAKNSSSGFVLEHDHQTETETST 122  
Db 60 VSDSGFCVSLSEEDDHLSSISGCGSSSETNEIATRLPF--SDLEAHEI-SETEIST 116

QY 123 FITSNFRKETSPPVSEGLGET-----TTMESSSATKRKQGVKRTPTAAEIEDLFSEL 175  
Db 117 LUTNFRKQGISSENIGETAEWDSATTMRDQKTEKKK-MEKSPTQAELEDDFFSAA 175

QY 176 ESPDDKKQFIEKYNFDIVNDEPLEGRYK 205  
Db 176 ERYE--QKRFTKYNDIVNDTPLEGRYQW 203

## RESULT 7

US-10-424-599-212181

Sequence 212181, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 212181

LENGTH: 176

TYPE: PRT

ORGANISM: Glycine max

FEATURE:

OTHER INFORMATION: Clone ID: PAT MRT3847\_33625C.1.pep

US-10-424-599-212181

Query Match 20.1%; Score 210.5; DB 15; Length 176;  
Best Local Similarity 34.0%; Pred. No. 3.3e-08;  
Matches 70; Conservative 28; Mismatches 67; Indels 41; Gaps 8;

QY 13 MSERKR-----BLAEASSTSFSPPLKTKLNDSSDSSPDSDHVIIVFAVSSSSVASSAALA 67  
Db 1 MGECKRCSLTIAAIEQPSSSQHSISKRTTAS-----FQLRSSDTQFPDPTIV 48

QY 68 SDECSVTIGGEESDQSSSISSGCGFTSESKEIAKNSSSGFVLEHDHQTETETSTF---- 123  
Db 49 SPEASVSTG-----TVVSGDFCSDR---SCCSSSHFKDL--HSVPDLQTKGQTVE 96

QY 124 -LTSNFRKETSPPVSEGLGETTTTMESSSATKRKQGVKRTPTAAEIEDLFSELESDDKK 182  
Db 97 DSTNRYKFPFLSLUSFGSDSESAKSSAAVRK-----LKTTPQAEIEEFAMAEKYE--R 149

QY 183 KQFIEKYNFDIVNDEPLEGRYKWDRL 208  
Db 150 KRFTEKYNFDIVRDLPLEGRYQWVRL 175

## RESULT 8

US-10-890-629-59

Sequence 59, Application US/10890629

Publication No. US2005004824A1

GENERAL INFORMATION:

APPLICANT: Savidge, Beth





```

RESULT 14
US-10-424-599-182928
; Sequence 182928, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 182928
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_136198C.1 pep
US-10-424-599-182928

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Query Match	16.5%	Score 172;	DB 15;	Length 205;
Best Local Similarity	30.7%;	Pred. No. 3.4e-05;		
Matches 63; Conservative	36;	Mismatches 74;	Indels 32;	Gaps 10.
Qy	20	LAEASSTFSPLKTKKLNLDSSSDPSHDVIVFAVSSSVASSAALASDECDSVTIGGEE	79	
Db	15	LAMEAVSSAEPSSKRRKLSINSTQEPK-----LSKTPRTSSSAVKPATVT---E	61	
Qy	80	SDQSS---ISSGGFTBSKEI-----AKNSSFGVD-----LEDHQIET-ETETSTFTFS	126	
Db	62	MVQVPSEMVQQRCLSTPSSIPASCSSNGSIGLDQDRIKLLDLIEVSAQVETSTCNGG	121	
Qy	127	N--FRKETSVPSEGLGTTTTMEMSSSATKRQPGVRKT-PTAAAEIEDLFSELESPPDKKK	183	
Db	122	HEIEREMKSSSE-LRENSQEPPEWINSHRVLSKAKAMPTLELEEFPAASEK-DIQK	178	
Qy	184	QFIETKYNFDIINDPELEGRYKWDRL	208	
Db	179	RFODRYNYDVKQVPLEGRYEWQL	203	

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RESULT 15
US-10-424-599-210190
; Sequence 210190, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 210190
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_3182C.1.pcp
US-10-424-599-210190

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Query Match      16.4%; Score 171.5; DB 15; Length 224;
Best Local Similarity 30.9%; Pred. No. 4.1e-05;
Matches 42; Conservative 29; Mismatches 54; Indels 11; Gaps 4;

Qy 77 GEESDQSSISGCGFTSESKEIAKNSSFG---VDLEDHQIETETETSTFTTSNFRKETS 133
Db 94 GLASERDNLNHNKDNLTILHNAEPQEAQSGFGENVLDFEGRERSTRESTPCSLIRSDTVRT 153

Qy 134 PVSEGLGTTTMESSSATKQKQGVK-TPTAAEIEDLSELESPPDDKKQKQIEKYNFD 192
Db 154 P-----GSTTPTCSAEAYRTEHAARQIPTSRWDEFFAEIEAQOKK--FIEKYNFD 206

Qy 193 IVNDEPLEGRYKWDRL 208
Db 207 PVNEKPLSGRYEWKL 222

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Search completed: September 30, 2005, 11:43:33  
Job time : 412 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 30, 2005, 10:08:22 ; Search time 24 Seconds  
(without alignments)  
837.888 Million cell updates/sec

Title: US-09-980-758A-8  
Perfect score: 1045  
Sequence: 1 PRDLKPNPREKKMSRKREL.....NFDIVNDEPLEGRYKWDRLX 209

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79: \*  
1: Pir1: \*  
2: Pir2: \*  
3: Pir3: \*  
4: Pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	346.5	33.2	195	2 H96532	hypothetical prote
2	177	16.9	209	2 T46140	hypothetical prote
3	175.5	16.8	191	2 T01132	cyclin-dependent k
4	168.5	16.1	196	2 T09968	cyclin-dependent k
5	156.5	15.0	500	2 S55785	nucleolar protein
6	138.5	13.3	406	2 S38170	SRP40 protein - ye
7	133.5	12.8	327	2 T00797	hypothetical prote
8	132.5	12.7	414	2 A39205	nuclear localizati
9	132.5	12.7	2271	2 F90073	hypothetical prote
10	121	11.6	536	2 T37544	hypothetical serin
11	120.5	11.5	1359	2 T34036	hypothetical prote
12	117.5	11.2	557	2 A96527	probable nuM1 prot
13	116.5	11.1	344	2 T40167	hypothetical prote
14	116.5	11.1	534	2 T39903	serine-rich protei
15	116	11.1	238	2 S77699	inner cell wall ma
16	116	11.1	1280	2 G96796	hypothetical prote
17	116	11.1	1312	2 T23088	vitellogenin I pre
18	113.5	10.9	611	2 T2456	hypothetical prote
19	113.5	10.9	1829	2 T24583	hypothetical prote
20	113	10.8	611	2 T06458	nucleolin homolog
21	113	10.8	916	2 S22864	DNA topoisomerase
22	112.5	10.8	725	2 A41258	a-aggutinin core
23	112	10.7	273	2 T44657	protein GP80 limpo
24	112	10.7	3507	2 T34513	hypothetical prote
25	111	10.6	1217	2 S52714	sericin1B - silkw
26	110.5	10.6	1224	2 F96795	hypothetical prote
27	109.5	10.5	581	2 T24555	hypothetical prote
28	109.5	10.5	888	2 T46726	secreted acid phos
29	109.5	10.5	1230	2 T22458	hypothetical prote

30	109.5	10.5	1306	2 S25370	MSB2 protein - yea
31	109	10.4	327	2 S48416	hypothetical prote
32	109	10.4	503	2 S63257	probable membrane
33	109	10.4	550	2 T29919	hypothetical prote
34	109	10.4	551	2 S64314	probable membrane
35	109	10.4	604	2 T15091	hypothetical prote
36	109	10.4	1063	2 D88731	hypothetical prote
37	109	10.4	1094	2 T50651	AP3-complex beta-3
38	108	10.3	4776	2 E95206	cell wall surface
39	107.5	10.3	667	2 A40713	cylicin I - bovine
40	107.5	10.3	1072	2 A86827	hypothetical prote
41	107.5	10.3	2748	2 S57976	nuclear migration
42	107	10.2	630	2 A39344	tumor-associated m
43	107	10.2	631	2 I52257	episialin - mouse
44	107	10.2	1015	2 JC6552	DNA topoisomerase
45	107	10.2	1234	2 T31623	hypothetical prote

ALIGNMENTS

RESULT 1

H96532  
hypothetical protein F14J22.14 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: H96532  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: H96532  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-195 <STO>  
A:Cross-references: UNIPROT:Q9FX90; GB:AE005173; NID:g10120423; PIDN:AAG13048.1; GSPDB: C:Genetics:  
A:Gene: F14J22.14  
A:Map position: 1

Query Match 33.2%; Score 346.5; DB 2; Length 195;  
Best Local Similarity 45.4%; Pred. No. 3e-16;  
Matches 93; Conservative 27; Mismatches 58; Indels 27; Gaps 10;

QY	13	MSERKRELAEEASSTFSPLKTKLNDSD--SSPDSDHVIIVFVSSSSSVASSAALASDE	70
DB	1	MSEYFKRDSVEG---SNIKRWLDDDDVLRSTR-----TLSSSSSSSLAVSVSDS	51
QY	71	---CSVTIGGEESDQ-SSSISSGCTFSKEIAKNSSFGVDLEDHQIETETETFTITS	126
DB	52	GGFCSVALSEEDDHLSSISSGCSSTNEIATLPF--SDLEAHEI-SETEISTLLTN	108
QY	127	NFRKETSVPSEGLGT-----TIEMESSATKRQKQGVKRTPTAAETEDLSELESPPD	180
DB	109	NFRKQGISSENGLGTAEKMSATTEMRDQRKTEKKK-MEKSPTQALDFFSAAREY-	166
QY	181	KKQFIEKYNFDIVNDEPLEGRYKW	205
DB	167	-QKRFTKYNFDIVNDEPLEGRYQW	190

RESULT 2

T46140  
hypothetical protein T3A5.10 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 09-Jul-2004



A;Cross-references: UNIPROT:P41891; EMBL:Z48166; MID:g663261; PIDN:CAA88179.1; PID:g6633333  
R;VanHoy, R.W.; Wise, J.A.  
Curr. Genet. 29, 307-315, 1996  
A;Title: Molecular analysis of a novel Schizosaccharomyces pombe gene containing two RNF  
A;Reference number: S68083; MUID:96171513; PMID:8598051  
A;Accession: S68087  
A;Status: nucleic acid sequence not shown; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 374-407 <VAN>  
R;Brown, D.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.  
submitted to the EMBL Data Library, September 1997  
A;Reference number: Z21733  
A;Accession: T37634  
A;Status: preliminary; translated from GB/EMBL/DDBB  
A;Molecule type: DNA  
A;Residues: 1-338, 'S', 340-500 <BRO>  
A;Cross-references: EMBL:Z99091; PIDN:CAB11772.1; GSPDB:GN00066; SPDB:SPAC13F5.09  
A;Experimental source: strain 972h-; cosmid c13F5  
C;Genetics:  
A;Gene: gar2; SPDB:SPAC13F5.09  
A;Map position: 1  
C;Superfamily: ribonucleoprotein repeat homology  
F;264-331/Domain: ribonucleoprotein repeat homology <RNM1>  
F;367-433/Domain: ribonucleoprotein repeat homology <RNM2>

Query Match 15.0%; Score 156.5; DB 2; Length 500;  
Best Local Similarity 29.5%; Pred. No. 0.0035;  
Matches 57; Conservative 37; Mismatches 74; Indels 25; Gaps 6;

Qy 1 PRDLKPNRKXKXERKELAEASSTFSPLKTKLNDSSDPDSDHVIIVAVSSSV 60  
Db 64 PEPFKSVKKQKXKKKBESSSESSSESSSESSSESSSESSSESSSESSSESSSESSSE 116  
Qy 61 ASSAAALASDCSVTIGGEESDQSSSISSGCTSESKEIA-----KNSSSFGVDLEDH 114  
Db 117 SSS---SESEEVIVKTEKKSSSSSSSSSSSESESESESESESESESESESSSSSS 173  
Qy 115 ETETSTFTTISNFR---KETSPVSEGLGTTTTMESSSATKRKQPGVARTPTAAIEDL 171  
Db 174 ESESESSSSSE 228  
Qy 172 FSELESPDDKKQ 184  
Db 229 -SESSSEDEKKR 240

RESULT 6  
SRP40 protein - yeast (Saccharomyces cerevisiae)  
N;Alternate names: protein YKR092C; protein YKR412a  
C;Species: Saccharomyces cerevisiae  
C;Date: 03-May-1994 #sequence revision 03-May-1994 #text\_change 09-Jul-2004  
C;Accession: S38170; S40645; S37702  
R;Baladron, V.; Ballesta, J.P.G.; Bou, G.; del Rey, F.; Garcia-Cantalejo, J.  
submitted to the Protein Sequence Database, March 1994  
A;Reference number: S38158  
A;Accession: S38170  
A;Molecule type: DNA  
A;Residues: 1-406 <BAL>  
A;Cross-references: UNIPROT:P32583; EMBL:Z28317; MID:g486580; PID:g486581; MIPS:YKR092C  
A;Experimental source: strain S288C  
R;Bou, G.; Esteban, P.F.; Baladron, V.; Gonzalez, G.A.; Cantalejo, J.G.; Remacha, M.; Ji  
Yeast 9, 1349-1354, 1993  
A;Title: The complete sequence of a 15 820 bp segment of Saccharomyces cerevisiae chromo  
A;Reference number: S40644; MUID:94205265; PMID:8154186  
A;Accession: S40645  
A;Molecule type: DNA  
A;Residues: 1-406 <BOU>  
A;Cross-references: EMBL:X73541; MID:g450550; PIDN:CRAA51946.1; PID:g450552  
A;Experimental source: strain S288C  
R;Lalo, D.; Carles, C.; Sentenac, A.; Thuriaux, P.  
submitted to the EMBL Data Library, May 1993  
A;Description: Interactions between three common subunits of yeast RNA polymerases I and

Qy 98 IAKNSSFG---VDLEPHQIET---ETETSTFTISNPKK--TSPVSEG-----LGETTT 144  
          ::|||::      ::|||::      ::|||::      ::|||::      :  
Db 175 ---KDPTGQNFFDLEBEHTQSFRTRTTPCSLIIRPEIMTPGSSTKLNICVSSESQ 231  
          ::|||::      ::|||::      ::|||::      ::|||::      :  
Qy 145 EMSSSATKKRQPGVKRTPTAAEIEDLFSESPDDKKQFIK----- 188  
          ::|||::      ::|||::      ::|||::      ::|||::      :  
Db 232 REDLSKSHRRR-----PTPDEMEFFSGAE--EEQQKFIEKYVPFRFICSVLLVMSF 283  
          |||||::|||::      ::|||::      ::|||::      ::|||::      :  
Qy 189 -----YNFOIVNDEPLEGRYKWDRL 208  
          |||||::|||::      ::|||::      ::|||::      ::|||::      :  
Db 284 QFVLFFSGLSLMVSNFSFRYNFDPNNEQPLGREFTWKV 325  
          |||||::|||::      ::|||::      ::|||::      ::|||::      :  
  
RESULT 8  
A39205  
nuclear localization sequence-binding protein NSR1 - yeast (*Saccharomyces cerevisiae*)  
N;Alternate names: nucleolar protein NSR1; p67 protein; protein G7001; protein YGR159c;  
C;Species: *Saccharomyces cerevisiae*  
C;Date: 14-Feb-1992 #sequence\_revision 14-Feb-1992 #text\_change 09-Jul-2004  
C;Accession: A39205; PC2395; S60450; S64468; S64470  
R;Lee, W.C.; Xue, Z.; Melese, T.  
J. Cell Biol. 113, 1-12, 1991.  
A;Title: The NSR1 gene encodes a protein that specifically binds nuclear localization se  
A;Reference number: A39205; MUID:91177946; PMID:1706724  
A;Accession: A39205  
A:Molecule type: DNA  
A;Residues: 1-414 <LEE>  
A;Cross-references: UNIPROT:P27476; GB:X57185; NID:g4057; PIDN:CAA0472.1; PID:g4058  
R;Gamberi, C.; Contreas, G.; Romanelli, M.G.; Morandi, C.  
Gene 148, 59-66, 1994  
A;Title: Analysis of the yeast Nsr1 gene and protein domain comparison between Nsr1 and  
A;Reference number: PC2395; MUID:95011659; PMID:7926838  
A;Accession: PC2395  
A:Molecule type: mRNA  
A;Residues: 155-414 <GAM>  
A;Cross-references: EMBL:X57185  
A;Note: The authors translated the codon TTC for residue 188 as Arg, GGT for residue 254  
R;Skala, J.; Nawrocki, A.; Goffeau, A.  
Yeast 11, 1421-1427, 1995  
A;Title: The sequence of a 27 kb segment on the right arm of chromosome VII from *Sacchar*  
. A;Reference number: S60435; MUID:96158062; PMID:8585325  
A;Accession: S60450  
A;Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A;Residues: 1-414 <SKA>  
A;Cross-references: EMBL:X85807; NID:g1045249; PIDN:CAAS9817.1; PID:g1045265  
R;Van Dyck, L.; Skala, J.; de Wergifosse, P.; Purnelle, B.; Tallia, E.; Nawrocki, A.; Del  
submitted to the Protein Sequence Database, May 1996  
A;Reference number: S64428  
A;Accession: S64468  
A:Molecule type: DNA  
A;Residues: 1-414 <VAN>  
A;Cross-references: EMBL:Z72944; NID:gl323270; PIDN:CAA97173.1; PID:e243542; PID:gl32327  
A;Experimental source: strain S288C  
R;Rieger, M.; Mueller-Auer, S.; Brueckner, M.; Schaefer, M.  
submitted to the Protein Sequence Database, May 1996  
A;Reference number: S64071  
A;Accession: S64470  
A:Molecule type: DNA  
A;Residues: 1-188 <RIE>  
A;Cross-references: EMBL:Z72944; MIPS:YGR159c  
A;Experimental source: strain S288C  
C;Genetics:  
A;Gene: SGD:NSR1  
A;Cross-references: SGD:S0003391; MIPS:YGR159c  
A;Map position: 7R  
C;Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleoprotein  
C;Keywords: DNA binding; nucleus; RNA binding  
F:169-236/Domain: ribonucleoprotein repeat homology <RRM1>  
F:268-336/Domain: ribonucleoprotein repeat homology <RRM2>

Query Match 12.7%; Score 132.5; DB 2; Length 414;  
Best Local Similarity 29.3%; Pred. No. 0.11;  
Matches 61; Conservative 25; Mismatches 73; Indels 49; Gaps 9;

QY 7 NPREKMSERKRELAEASSTSFPLKTKLNDSSDSDSPSHDVIVFAVSSSVASSAAL 66  
Db 10 NKKEVKASKQAKR--EKAVVSS-----SSESSSS-----SSSESSESE 50

QY 67 ASDECVTIGGESDOSSGCFTSES-----KEIAKNSSSGVD-LEDHQIETET 120  
Db 51 SESESSSSSDSESSSSSS--DSPEATKKEESKDSSSSDSSDEEEEEKKEE 107

QY 121 STPITNFRKETSPVEGLGETTEMESSATKRKGVRKTPTAAIEIDLFELESPDD 180  
Db 108 TKKEESKESSSDSSSSSDSDSEKESGDKRKKS-----EDAEEDDEESS 155

QY 181 KKKQFTEKYNFDVINDEP---LEGRYKW 205  
Db 156 NKKQKNEE-----TEEPATIFVGRLSW 177

RESULT 9  
F90073  
hypothetical protein SA2447 [imported] - Staphylococcus aureus (strain N315)  
C:Species: Staphylococcus aureus  
C>Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C:Accession: F90073  
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui,  
ma, A.; Mizutani-Taito, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekim  
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.  
Lancet 357, 1225-1240, 2001  
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.  
A:Reference number: A89758; UID:21311952; PMID:11418146  
A:Accession: F90073  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-2271 <KUR>  
A:Cross-references: UNIPROT:Q99QY4; GB:BA000018; PID:g13702612; PIDN:BAB43752.1  
A:Experimental source: strain N315  
C:Genetics:  
A:Gene: SA2447

Query Match 12.7%; Score 132.5; DB 2; Length 2271;  
Best Local Similarity 25.8%; Pred. No. 0.8;  
Matches 47; Conservative 35; Mismatches 89; Indels 11; Gaps 4;

QY 14 SERKRELAERASTSFPLKTKLNDSSDSDSPSHDVIVFAVS-----SSSVASSAALAS 68  
Db 1024 SDGKSMGVSSMGTSSQGSSTSESLSDSQSTDSDSKSLSLTSSQSGSTSTSTSTASVRT 1083

QY 69 DECSVTIGGESDOSSGCFTSESKEIAKNSSSGVDLEDHQIETET---ETSTFI 124  
Db 1084 SESQSTSGMSAQSDSMSTISFSDSTSDSKASTASSEISQSASTTSFGSVSTSTSL 1143

QY 125 -TSNFRKETSPVEGLGETTEMESSATKRKGVRKTPTAAIEIDL-FSELESPPDKK 182  
Db 1144 STNSERTSTVSDSTSLTSESDSIESTSTSDSTISEAISASESTISLSENSTSDSE 1203

QY 183 KQ 184  
Db 1204 SQ 1205

RESULT 10  
T37544  
hypothetical serine-rich protein - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C:Accession: T37544  
R;McLean, J.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.  
submitted to the EMBL Data Library, September 1997  
A:Reference number: Z21722  
A:Accession: T37544

[illegible]

C;Accession: A96527  
R:Theologas, A.; Ecker, J.R.: Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C  
C.A.; Li, J.H.; Li, Y.T.; Lin, X.; Liu, Z.A.; Luo, J.S.; Maiti, R.; Marziani  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: AB6141; MID:21016719; PMID:11130712

A:Accession: A96527  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-557 <STO>  
A:Cross-references: UNIPROT:Q9FVQI; GB:AEO05173; NID:g11094815; PIDN:AAG29744.1; GSPDB:  
C:Genetics:  
A:Gene: F2TK7.6  
A:Map position: 1

Query Match                  11.2%; Score 117.5; DB 2; Length 557;  
Best Local Similarity    24.9%; Pred. No. 1.5;  
Matches         51; Conservative      27; Mismatches    70; Indels    57; Gaps    7;

Qy         1 PDLPKNPKRMSEKRELAEASSTSFSPLKK-----TKLNDSDSSPD 46  
| | : : : : : : : : : : : : : : : : : :  
Db        141 PAAAKNGSVK---AKGESSEDSSDEPAKKAIAKPAAKDSSDDSDSDES 197

Qy         47 SHDVIVPANSVSASAALADSCVTTCGGESDSSISSCGFTSESKEIKNSSFG 106  
| : : : : : : : : : : : : : : : : : :  
Db        198 EKPATKKAAPAAKAAASSDSDEDSS----DEEDEKPAKKAOTKASK---KSSDES 250

Qy         107 VLLEDHQIETETTSFTITSFNFRKETSPVSEGIGLTTEWESSATKRQPGRVKTPTA- 165  
| : : : : : : : : : : : : : : : : : :  
Db        251 SESEEDEEETP-----KKKSDEV-----EMVD AEKSSAQPTTSPAAG 294

Qy         166 -----AEIEDLFSE 174  
| : : : : : : : : : : : : : : : : : :  
Db        295 GSXTLFAANLSFNIERADVNPPEKE 319

RESULT 13

T40167  
hypothetical protein SPBC30B4.01c - fission yeast (*Schizosaccharomyces pombe*) (fragment  
C;Species: Schizosaccharomycetes pombe)  
C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C;Accession: T40167; T40374  
R:Lynne, M.; Rajandream, M.A.; Barrell, B.G.; Hilbert, H.; Duesterhoeft, A.  
submitted to the EMBL Data Library, August 1998  
A:Reference number: Z21909  
A:Accession: T40167  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-344 <LYN>  
A:CROSS-references: UNIPROT:P87179; EMBL:AL031262; PIDN:CAA20314.1; GSPDB:GN00067; SPDB:  
A:Experimental source: strain 972H; cosmid c30B4  
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Hilbert, H.; Duesterhoeft, A.  
submitted to the EMBL Data Library, December 1998  
A:Reference number: Z21923  
A:Accession: T40374  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 16-344 <WOOD>  
A:CROSS-references: EMBL:Z95620; PIDN:CA09116.1; GSPDB:GN00067; SPDB:SPBC3D6.14C  
A:Experimental source: strain 972H; cosmid c3D6  
C:Genetics:  
A:Gene: SPBC3D5.14C; SPDB:SPBC30B4.01c; SPDB:SPBC3D6.14C  
A:Map position: 2

Query Match                  11.1%; Score 116.5; DB 2; Length 344;  
Best Local Similarity    32.1%; Pred. No. 1;  
Matches         42; Conservative      19; Mismatches    57; Indels    13; Gaps    2;

RESULT 12  
A96527  
probable num1 protein [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Mar-2001 #sequence revision 02-Mar-2001 #text change 09-Jul-2004

